(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
5 April 2001 (05.04.2001)

PCT

(10) International Publication Number
WO 01/23558 A2

(51) International Patent Classification[7]: C12N 15/12, C07K 14/705, C12Q 1/68, G01N 33/50, A01K 67/027

(21) International Application Number: PCT/US00/25610

(22) International Filing Date:
19 September 2000 (19.09.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/156,624	28 September 1999 (28.09.1999)	US
60/156,625	28 September 1999 (28.09.1999)	US
60/168,611	2 December 1999 (02.12.1999)	US
60/168,613	2 December 1999 (02.12.1999)	US
60/168,614	2 December 1999 (02.12.1999)	US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

US	60/156,624 (CIP)
Filed on	28 September 1999 (28.09.1999)
US	60/156,625 (CIP)
Filed on	28 September 1999 (28.09.1999)
US	60/168,614 (CIP)
Filed on	2 December 1999 (02.12.1999)
US	60/168,611 (CIP)
Filed on	2 December 1999 (02.12.1999)
US	60/168,613 (CIP)
Filed on	2 December 1999 (02.12.1999)

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(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European

[Continued on next page]

(54) Title: SECRETORY MOLECULES

(57) Abstract: The present invention provides purified secretory polynucleotides (sptm). Also encompassed are the polypeptides (SPTM) encoded by sptm. The invention also provides for the use of sptm, or complements, oligonucleotides, or fragments thereof in diagnostic assays. The invention further provides for vectors and host cells containing sptm for the expression of SPTM. The invention additionally provides for the use of isolated and purified SPTM to induce antibodies and to screen libraries of compounds and the use of anti-SPTM antibodies in diagnostic assays. Also provided are microarrays containing sptm and methods of use.

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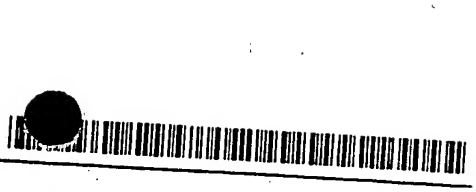

patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

— *Without international search report and to be republished upon receipt of that report.*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

SECRETORY MOLECULES

TECHNICAL FIELD

The present invention relates to secretory molecules and to the use of these sequences in the diagnosis, study, prevention, and treatment of diseases associated with, as well as effects of exogenous compounds on, cell signaling and the expression of secretory molecules.

BACKGROUND OF THE INVENTION

Protein transport and secretion are essential for cellular function. Protein transport is mediated by a signal peptide located at the amino terminus of the protein to be transported or secreted. The signal peptide is comprised of about ten to twenty hydrophobic amino acids which target the nascent protein from the ribosome to a particular membrane bound compartment such as the endoplasmic reticulum (ER). Proteins targeted to the ER may either proceed through the secretory pathway or remain in any of the secretory organelles such as the ER, Golgi apparatus, or lysosomes. Proteins that transit through the secretory pathway are either secreted into the extracellular space or retained in the plasma membrane. Proteins that are retained in the plasma membrane contain one or more transmembrane domains, each comprised of about 20 hydrophobic amino acid residues. Proteins that are secreted from the cell are generally synthesized as inactive precursors that are activated by post-translational processing events during transit through the secretory pathway. Such events include glycosylation, proteolysis, and removal of the signal peptide by a signal peptidase. Other events that may occur during protein transport include chaperone-dependent unfolding and folding of the nascent protein and interaction of the protein with a receptor or pore complex. Examples of secretory proteins with amino terminal signal peptides are discussed below and include proteins with important roles in cell-to-cell signaling. Such proteins include transmembrane receptors and cell surface markers, extracellular matrix molecules, cytokines, hormones, growth and differentiation factors, neuropeptides, vasomediators, ion channels, transporters/pumps, and proteases. (Reviewed in Alberts, B. et al. (1994) Molecular Biology of The Cell, Garland Publishing, New York, NY, pp. 557-560, 582-592.)

G-protein coupled receptors (GPCRs) comprise a superfamily of integral membrane proteins which transduce extracellular signals. Not all GPCRs contain N-terminal signal peptides. GPCRs include receptors for biogenic amines such as dopamine, epinephrine, histamine, glutamate (metabotropic-type), acetylcholine (muscarinic-type), and serotonin; for lipid mediators of inflammation such as prostaglandins, platelet activating factor, and leukotrienes; for peptide hormones such as calcitonin, C5a anaphylatoxin, follicle stimulating hormone, gonadotropin releasing hormone, neurokinin, oxytocin, and thrombin; and for sensory signal mediators such as retinal photopigments and olfactory stimulatory molecules. The structure of these highly conserved receptors consists of seven

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JC10 Rec'd PCT/PTO 27 MAR 2002
PCT/US00/25610

hydrophobic transmembrane regions, cysteine disulfide bridges between the second and third extracellular loops, an extracellular N-terminus, and a cytoplasmic C-terminus. The N-terminus interacts with ligands, the disulfide bridges interact with agonists and antagonists, and the large third intracellular loop interacts with G proteins to activate second messengers such as cyclic AMP, phospholipase C, inositol triphosphate, or ion channels. (Reviewed in Watson, S. and Arkinstall, S. (1994) The G-protein Linked Receptor Facts Book, Academic Press, San Diego, CA, pp. 2-6; and Bolander, F.F. (1994) Molecular Endocrinology, Academic Press, San Diego, CA, pp. 162-176.)

Other types of receptors include cell surface antigens identified on leukocytic cells of the immune system. These antigens have been identified using systematic, monoclonal antibody (mAb)-based "shot gun" techniques. These techniques have resulted in the production of hundreds of mAbs directed against unknown cell surface leukocytic antigens. These antigens have been grouped into "clusters of differentiation" based on common immunocytochemical localization patterns in various differentiated and undifferentiated leukocytic cell types. Antigens in a given cluster are presumed to identify a single cell surface protein and are assigned a "cluster of differentiation" or "CD" designation. Some of the genes encoding proteins identified by CD antigens have been cloned and verified by standard molecular biology techniques. CD antigens have been characterized as both transmembrane proteins and cell surface proteins anchored to the plasma membrane via covalent attachment to fatty acid-containing glycolipids such as glycosylphosphatidylinositol (GPI). (Reviewed in Barclay, A. N. et al. (1995) The Leucocyte Antigen Facts Book, Academic Press, San Diego, CA, pp. 17-20.)

Matrix proteins (MPs) are transmembrane and extracellular proteins which function in formation, growth, remodeling, and maintenance of tissues and as important mediators and regulators of the inflammatory response. The expression and balance of MPs may be perturbed by biochemical changes that result from congenital, epigenetic, or infectious diseases. In addition, MPs affect leukocyte migration, proliferation, differentiation, and activation in the immune response. MPs are frequently characterized by the presence of one or more domains which may include collagen-like domains, EGF-like domains, immunoglobulin-like domains, and fibronectin-like domains. In addition, MPs may be heavily glycosylated and may contain an Arginine-Glycine-Aspartate (RGD) tripeptide motif which may play a role in adhesive interactions. MPs include extracellular proteins such as fibronectin, collagen, galectin, vitronectin and its proteolytic derivative somatomedin B; and cell adhesion receptors such as cell adhesion molecules (CAMs), cadherins, and integrins. (Reviewed in Ayad, S. et al. (1994) The Extracellular Matrix Facts Book, Academic Press, San Diego, CA, pp. 2-16; Ruoslahti, E. (1997) Kidney Int. 51:1413-1417; Sjaastad, M.D. and Nelson, W.J. (1997) BioEssays 19:47-55.)

Cytokines are secreted by hematopoietic cells in response to injury or infection. Interleukins,

Ion channels, ion pumps, and transport proteins mediate the transport of molecules across cellular membranes. Transport can occur by a passive, concentration-dependent mechanism or can be linked to an energy source such as ATP hydrolysis. Symporters and antiporters transport ions and small molecules such as amino acids, glucose, and drugs. Symporters transport molecules and ions unidirectionally, and antiporters transport molecules and ions bidirectionally. Transporter superfamilies include facilitative transporters and active ATP-binding cassette transporters which are involved in multiple-drug resistance and the targeting of antigenic peptides to MHC Class I molecules. These transporters bind to a specific ion or other molecule and undergo a conformational change in order to transfer the ion or molecule across the membrane. (Reviewed in Alberts, B. et al. (1994) Molecular Biology of The Cell, Garland Publishing, New York, NY, pp. 523-546.)

Ion channels are formed by transmembrane proteins which create a lined passageway across the membrane through which water and ions, such as Na^+, K^+, Ca^{2+}, and Cl^-, enter and exit the cell. For example, chloride channels are involved in the regulation of the membrane electric potential as well as absorption and secretion of ions across the membrane. Chloride channels also regulate the internal pH of membrane-bound organelles.

Ion pumps are ATPases which actively maintain membrane gradients. Ion pumps are classified as P, V, or F according to their structure and function. All have one or more binding sites for ATP in their cytosolic domains. The P-class ion pumps include Ca^{2+} ATPase and Na^+/K^+ ATPase and function in transporting H^+, Na^+, K^+, and Ca^{2+} ions. P-class pumps consist of two α and two β transmembrane subunits. The V- and F-class ion pumps have similar structures but transport only H^+. F class H^+ pumps mediate transport across the membranes of mitochondria and chloroplasts, while V-class H^+ pumps regulate acidity inside lysosomes, endosomes, and plant vacuoles.

A family of structurally related intrinsic membrane proteins known as facilitative glucose transporters catalyze the movement of glucose and other selected sugars across the plasma membrane. The proteins in this family contain a highly conserved, large transmembrane domain comprised of 12 α-helices, and several weakly conserved, cytoplasmic and exoplasmic domains. (Pessin, J. E., and Bell, G.I. (1992) Annu. Rev. Physiol. 54:911-930.)

Amino acid transport is mediated by Na^+ dependent amino acid transporters. These transporters are involved in gastrointestinal and renal uptake of dietary and cellular amino acids and in neuronal reuptake of neurotransmitters. Transport of cationic amino acids is mediated by the system y+ family and the cationic amino acid transporter (CAT) family. Members of the CAT family share a high degree of sequence homology, and each contains 12-14 putative transmembrane domains. (Ito, K. and Groudine, M. (1997) J. Biol. Chem. 272:26780-26786.)

Hormones are secreted molecules that travel through the circulation and bind to specific receptors on the surface of, or within, target cells. Although they have diverse biochemical compositions

neurotrophins, growth factors, interferons, and chemokines all define cytokine families that work in conjunction with cellular receptors to regulate cell proliferation and differentiation. In addition, cytokines effect activities such as leukocyte migration and function, hematopoietic cell proliferation, temperature regulation, acute response to infection, tissue remodeling, and apoptosis.

Chemokines, in particular, are small chemoattractant cytokines involved in inflammation, leukocyte proliferation and migration, angiogenesis and angiostasis, regulation of hematopoiesis, HIV infectivity, and stimulation of cytokine secretion. Chemokines generally contain 70-100 amino acids and are subdivided into four subfamilies based on the presence of conserved cysteine-based motifs. (Callard, R. and Gearing, A. (1994) The Cytokine Facts Book, Academic Press, New York, NY, pp. 181-190, 210-213, 223-227.)

Growth and differentiation factors are secreted proteins which function in intercellular communication. Some factors require oligomerization or association with MPs for activity. Complex interactions among these factors and their receptors trigger intracellular signal transduction pathways that stimulate or inhibit cell division, cell differentiation, cell signaling, and cell motility. Most growth and differentiation factors act on cells in their local environment (paracrine signaling). There are three broad classes of growth and differentiation factors. The first class includes the large polypeptide growth factors such as epidermal growth factor, fibroblast growth factor, transforming growth factor, insulin-like growth factor, and platelet-derived growth factor. The second class includes the hematopoietic growth factors such as the colony stimulating factors (CSFs). Hematopoietic growth factors stimulate the proliferation and differentiation of blood cells such as B-lymphocytes, T-lymphocytes, erythrocytes, platelets, eosinophils, basophils, neutrophils, macrophages, and their stem cell precursors. The third class includes small peptide factors such as bombesin, vasopressin, oxytocin, endothelin, transferrin, angiotensin II, vasoactive intestinal peptide, and bradykinin which function as hormones to regulate cellular functions other than proliferation.

Growth and differentiation factors play critical roles in neoplastic transformation of cells in vitro and in tumor progression in vivo. Inappropriate expression of growth factors by tumor cells may contribute to vascularization and metastasis of tumors. During hematopoiesis, growth factor misregulation can result in anemias, leukemias, and lymphomas. Certain growth factors such as interferon are cytotoxic to tumor cells both in vivo and in vitro. Moreover, some growth factors and growth factor receptors are related both structurally and functionally to oncoproteins. In addition, growth factors affect transcriptional regulation of both proto-oncogenes and oncosuppressor genes. (Reviewed in Pimentel, E. (1994) Handbook of Growth Factors, CRC Press, Ann Arbor, MI, pp. 1-9.)

Proteolytic enzymes or proteases either activate or deactivate proteins by hydrolyzing peptide bonds. Proteases are found in the cytosol, in membrane-bound compartments, and in the extracellular space. The major families are the zinc, serine, cysteine, thiol, and carboxyl proteases.

e) an RNA equivalent of a) through d). In one alternative, the polynucleotide comprises a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63. In another alternative, the polynucleotide comprises at least 60 contiguous nucleotides of a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63; b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63; c) a polynucleotide sequence complementary to a); d) a polynucleotide sequence complementary to b); and e) an RNA equivalent of a) through d). The invention further provides a composition for the detection of expression of secretory polynucleotides comprising at least one isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63; b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63; c) a polynucleotide sequence complementary to a); d) a polynucleotide sequence complementary to b); and e) an RNA equivalent of a) through d); and a detectable label.

The invention also provides a method for detecting a target polynucleotide in a sample, said target polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63; b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63; c) a polynucleotide sequence complementary to a); d) a polynucleotide sequence complementary to b); and e) an RNA equivalent of a) through d). The method comprises a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide, and b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof. In one alternative, the probe comprises at least 30 contiguous nucleotides. In another alternative, the probe comprises at least 60 contiguous nucleotides.

The invention further provides a recombinant polynucleotide comprising a promoter sequence operably linked to an isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63; b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63; c) a polynucleotide sequence complementary to a); d) a polynucleotide sequence complementary to b); and e) an RNA equivalent of a) through d). In one alternative, the invention provides a cell transformed with the recombinant polynucleotide. In another alternative, the invention provides a transgenic organism

and mechanisms of action, hormones can be grouped into two categories. One category includes small lipophilic hormones that diffuse through the plasma membrane of target cells, bind to cytosolic or nuclear receptors, and form a complex that alters gene expression. Examples of these molecules include retinoic acid, thyroxine, and the cholesterol-derived steroid hormones such as progesterone, estrogen, testosterone, cortisol, and aldosterone. The second category includes hydrophilic hormones that function by binding to cell surface receptors that transduce signals across the plasma membrane. Examples of such hormones include amino acid derivatives such as catecholamines and peptide hormones such as glucagon, insulin, gastrin, secretin, cholecystokinin, adrenocorticotropic hormone, follicle stimulating hormone, luteinizing hormone, thyroid stimulating hormone, and vasopressin. (See, for example, Lodish et al. (1995) Molecular Cell Biology, Scientific American Books Inc., New York, NY, pp. 856-864.)

Neuropeptides and vasomediators (NP/VM) comprise a large family of endogenous signaling molecules. Included in this family are neuropeptides and neuropeptide hormones such as bombesin, neuropeptide Y, neurotensin, neuromedin N, melanocortins, opioids, galanin, somatostatin, tachykinins, urotensin II and related peptides involved in smooth muscle stimulation, vasopressin, vasoactive intestinal peptide, and circulatory system-borne signaling molecules such as angiotensin, complement, calcitonin, endothelins, formyl-methionyl peptides, glucagon, cholecystokinin and gastrin. NP/VMs can transduce signals directly, modulate the activity or release of other neurotransmitters and hormones, and act as catalytic enzymes in cascades. The effects of NP/VMs range from extremely brief to long-lasting. (Reviewed in Martin, C. R. et al. (1985) Endocrine Physiology, Oxford University Press, New York, NY, pp. 57-62.)

The discovery of new secretory molecules satisfies a need in the art by providing new compositions which are useful in the diagnosis, study, prevention, and treatment of diseases associated with, as well as effects of exogenous compounds on, cell signaling and the expression of secretory molecules.

SUMMARY OF THE INVENTION

The present invention relates to nucleic acid sequences comprising human polynucleotides encoding secretory polypeptides that contain signal peptides and/or transmembrane domains. These human polynucleotides (sptm) as presented in the Sequence Listing uniquely identify partial or full length genes encoding structural, functional, and regulatory polypeptides involved in cell signaling.

The invention provides an isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63; b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63; c) a polynucleotide sequence complementary to a); d) a polynucleotide sequence complementary to b); and

contiguous nucleotides of a polynucleotide comprising a polynucleotide sequence selected from the group consisting of i) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63; ii) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63; iii) a polynucleotide sequence complementary to i), iv) a polynucleotide sequence complementary to ii), and v) an RNA equivalent of i)-iv). Hybridization occurs under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence selected from the group consisting of i) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63; ii) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63; iii) a polynucleotide sequence complementary to i), iv) a polynucleotide sequence complementary to ii), and v) an RNA equivalent of i)-iv), and alternatively, the target polynucleotide comprises a fragment of a polynucleotide sequence selected from the group consisting of i-v above; c) quantifying the amount of hybridization complex; and d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

DESCRIPTION OF THE TABLES

Table 1 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with polynucleotide segments of each template sequence as defined by the indicated "start" and "stop" nucleotide positions. The reading frames of the polynucleotide segments are shown, and the polypeptides encoded by the polynucleotide segments constitute either signal peptide (SP) or transmembrane (TM) domains, as indicated.

Table 2 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with component sequence identification numbers (component IDs) corresponding to each template. The component sequences, which were used to assemble the template sequences, are defined by the indicated "start" and "stop" nucleotide positions along each template.

Table 3 shows the tissue distribution profiles for the templates of the invention.

Table 4 summarizes the bioinformatics tools which are useful for analysis of the polynucleotides of the present invention. The first column of Table 4 lists analytical tools, programs, and algorithms, the second column provides brief descriptions thereof, the third column presents appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate

comprising the recombinant polynucleotide. In a further alternative, the invention provides a method for producing a secretory polypeptide, the method comprising a) culturing a cell under conditions suitable for expression of the secretory polypeptide, wherein said cell is transformed with the recombinant polynucleotide, and b) recovering the secretory polypeptide so expressed.

The invention also provides a purified secretory polypeptide (SPTM) encoded by at least one polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63. Additionally, the invention provides an isolated antibody which specifically binds to the secretory polypeptide. The invention further provides a method of identifying a test compound which specifically binds to the secretory polypeptide, the method comprising the steps of a) providing a test compound; b) combining the secretory polypeptide with the test compound for a sufficient time and under suitable conditions for binding; and c) detecting binding of the secretory polypeptide to the test compound, thereby identifying the test compound which specifically binds the secretory polypeptide.

The invention further provides a microarray wherein at least one element of the microarray is an isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide comprising a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63; b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63; c) a polynucleotide sequence complementary to a); d) a polynucleotide sequence complementary to b); and e) an RNA equivalent of a) through d). The invention also provides a method for generating a transcript image of a sample which contains polynucleotides. The method comprises a) labeling the polynucleotides of the sample, b) contacting the elements of the microarray with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and c) quantifying the expression of the polynucleotides in the sample.

Additionally, the invention provides a method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a polynucleotide sequence selected from the group consisting of a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63; b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63; c) a polynucleotide sequence complementary to a); d) a polynucleotide sequence complementary to b); and e) an RNA equivalent of a) through d). The method comprises a) exposing a sample comprising the target polynucleotide to a compound, and b) detecting altered expression of the target polynucleotide.

The invention further provides a method for assessing toxicity of a test compound, said method comprising a) treating a biological sample containing nucleic acids with the test compound; b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20

Fv fragments, which are capable of binding the epitopic determinant. Antibodies that bind SPTM polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or peptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

"Antisense sequence" refers to a sequence capable of specifically hybridizing to a target sequence. The antisense sequence may include DNA, RNA, or any nucleic acid mimic or analog such as peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides having modified sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or oligonucleotides having modified bases such as 5-methyl cytosine, 2'-deoxyuracil, or 7-deaza-2'-deoxyguanosine.

"Antisense sequence" refers to a sequence capable of specifically hybridizing to a target sequence. The antisense sequence can be DNA, RNA, or any nucleic acid mimic or analog.

"Antisense technology" refers to any technology which relies on the specific hybridization of an antisense sequence to a target sequence.

A "bin" is a portion of computer memory space used by a computer program for storage of data, and bounded in such a manner that data stored in a bin may be retrieved by the program.

"Biologically active" refers to an amino acid sequence having a structural, regulatory, or biochemical function of a naturally occurring amino acid sequence.

"Clone joining" is a process for combining gene bins based upon the bins' containing sequence information from the same clone. The sequences may assemble into a primary gene transcript as well as one or more splice variants.

"Complementary" describes the relationship between two single-stranded nucleic acid sequences that anneal by base-pairing (5'-A-G-T-3' pairs with its complement 3'-T-C-A-5').

A "component sequence" is a nucleic acid sequence selected by a computer program such as PHRED and used to assemble a consensus or template sequence from one or more component sequences.

A "consensus sequence" or "template sequence" is a nucleic acid sequence which has been assembled from overlapping sequences, using a computer program for fragment assembly such as the GELVIEW fragment assembly system (Genetics Computer Group (GCG), Madison WI) or using a relational database management system (RDMS).

"Conservative amino acid substitutions" are those substitutions that, when made, least interfere with the properties of the original protein, i.e., the structure and especially the function of the protein is

the strength of a match between two sequences (the higher the score, the greater the homology between two sequences).

DETAILED DESCRIPTION OF THE INVENTION

Before the nucleic acid sequences and methods are presented, it is to be understood that this invention is not limited to the particular machines, methods, and materials described. Although particular embodiments are described, machines, methods, and materials similar or equivalent to these embodiments may be used to practice the invention. The preferred machines, methods, and materials set forth are not intended to limit the scope of the invention which is limited only by the appended claims.

The singular forms "a", "an", and "the" include plural reference unless the context clearly dictates otherwise. All technical and scientific terms have the meanings commonly understood by one of ordinary skill in the art. All publications are incorporated by reference for the purpose of describing and disclosing the cell lines, vectors, and methodologies which are presented and which might be used in connection with the invention. Nothing in the specification is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

Definitions

As used herein, the lower case "sptm" refers to a nucleic acid sequence, while the upper case "SPTM" refers to an amino acid sequence encoded by sptm. A "full-length" sptm refers to a nucleic acid sequence containing the entire coding region of a gene endogenously expressed in human tissue.

"Adjuvants" are materials such as Freund's adjuvant, mineral gels (aluminum hydroxide), and surface active substances (lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol) which may be administered to increase a host's immunological response.

"Allele" refers to an alternative form of a nucleic acid sequence. Alleles result from a "mutation," a change or an alternative reading of the genetic code. Any given gene may have none, one, or many allelic forms. Mutations which give rise to alleles include deletions, additions, or substitutions of nucleotides. Each of these changes may occur alone, or in combination with the others, one or more times in a given nucleic acid sequence. The present invention encompasses allelic sptm.

"Amino acid sequence" refers to a peptide, a polypeptide, or a protein of either natural or synthetic origin. The amino acid sequence is not limited to the complete, endogenous amino acid sequence and may be a fragment, epitope, variant, or derivative of a protein expressed by a nucleic acid sequence.

"Amplification" refers to the production of additional copies of a sequence and is carried out using polymerase chain reaction (PCR) technologies well known in the art.

"Antibody" refers to intact molecules as well as to fragments thereof, such as Fab, $F(ab')_2$, and

be preferentially selected from certain regions of a molecule. For example, a polypeptide fragment may comprise a certain length of contiguous amino acids selected from the first 250 or 500 amino acids (or first 25% or 50%) of a polypeptide as shown in a certain defined sequence. Clearly these lengths are exemplary, and any length that is supported by the specification, including the Sequence Listing and the figures, may be encompassed by the present embodiments.

A fragment of sptm comprises a region of unique polynucleotide sequence that specifically identifies sptm, for example, as distinct from any other sequence in the same genome. A fragment of sptm is useful, for example, in hybridization and amplification technologies and in analogous methods that distinguish sptm from related polynucleotide sequences. The precise length of a fragment of sptm and the region of sptm to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A fragment of SPTM is encoded by a fragment of sptm. A fragment of SPTM comprises a region of unique amino acid sequence that specifically identifies SPTM. For example, a fragment of SPTM is useful as an immunogenic peptide for the development of antibodies that specifically recognize SPTM. The precise length of a fragment of SPTM and the region of SPTM to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A "full length" nucleotide sequence is one containing at least a start site for translation to a protein sequence, followed by an open reading frame and a stop site, and encoding a "full length" polypeptide.

"Hit" refers to a sequence whose annotation will be used to describe a given template. Criteria for selecting the top hit are as follows: if the template has one or more exact nucleic acid matches, the top hit is the exact match with highest percent identity. If the template has no exact matches but has significant protein hits, the top hit is the protein hit with the lowest E-value. If the template has no significant protein hits, but does have significant non-exact nucleotide hits, the top hit is the nucleotide hit with the lowest E-value.

"Homology" refers to sequence similarity either between a reference nucleic acid sequence and at least a fragment of an sptm or between a reference amino acid sequence and a fragment of an SPTM.

"Hybridization" refers to the process by which a strand of nucleotides anneals with a complementary strand through base pairing. Specific hybridization is an indication that two nucleic acid sequences share a high degree of identity. Specific hybridization complexes form under defined annealing conditions, and remain hybridized after the "washing" step. The defined hybridization conditions include the annealing conditions and the washing step(s), the latter of which is particularly important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid probes that are not

conserved and not significantly changed by such substitutions. The table below shows amino acids which may be substituted for an original amino acid in a protein and which are regarded as conservative substitutions.

Original Residue	Conservative Substitution
Ala	Gly, Ser
Arg	His, Lys
Asn	Asp, Gln, His
Asp	Asn, Glu
Cys	Ala, Ser
Gln	Asn, Glu, His
Glu	Asp, Gln, His
Gly	Ala
His	Asn, Arg, Gln, Glu
Ile	Leu, Val
Leu	Ile, Val
Lys	Arg, Gln, Glu
Met	Leu, Ile
Phe	His, Met, Leu, Trp, Tyr
Ser	Cys, Thr
Thr	Ser, Val
Trp	Phe, Tyr
Tyr	His, Phe, Trp
Val	Ile, Leu, Thr

Conservative substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain.

"Deletion" refers to a change in either a nucleic or amino acid sequence in which at least one nucleotide or amino acid residue, respectively, is absent.

"Derivative" refers to the chemical modification of a nucleic acid sequence, such as by replacement of hydrogen by an alkyl, acyl, amino, hydroxyl, or other group.

The terms "element" and "array element" refer to a polynucleotide, polypeptide, or other chemical compound having a unique and defined position on a microarray.

"E-value" refers to the statistical probability that a match between two sequences occurred by chance.

A "fragment" is a unique portion of sptm or SPTM which is identical in sequence to but shorter in length than the parent sequence. A fragment may comprise up to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For example, a fragment may comprise from 10 to 1000 contiguous amino acid residues or nucleotides. A fragment used as a probe, primer, antigen, therapeutic molecule, or for other purposes, may be at least 5, 10, 15, 16, 20, 25, 30, 40, 50, 60, 75, 100, 150, 250 or at least 500 contiguous amino acid residues or nucleotides in length. Fragments may

multiple restriction enzyme sites and to provide for the use of enzymes which leave 5' or 3' overhangs (e.g., BamHI, EcoRI, and HindIII) and those which provide blunt ends (e.g., EcoRV, SnaBI, and StuI).

"Naturally occurring" refers to an endogenous polynucleotide or polypeptide that may be isolated from viruses or prokaryotic or eukaryotic cells.

"Nucleic acid sequence" refers to the specific order of nucleotides joined by phosphodiester bonds in a linear, polymeric arrangement. Depending on the number of nucleotides, the nucleic acid sequence can be considered an oligomer, oligonucleotide, or polynucleotide. The nucleic acid can be DNA, RNA, or any nucleic acid analog, such as PNA, may be of genomic or synthetic origin, may be either double-stranded or single-stranded, and can represent either the sense or antisense (complementary) strand.

"Oligomer" refers to a nucleic acid sequence of at least about 6 nucleotides and as many as about 60 nucleotides, preferably about 15 to 40 nucleotides, and most preferably between about 20 and 30 nucleotides, that may be used in hybridization or amplification technologies. Oligomers may be used as, e.g., primers for PCR, and are usually chemically synthesized.

"Operably linked" refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Generally, operably linked DNA sequences may be in close proximity or contiguous and, where necessary to join two protein coding regions, in the same reading frame.

"Peptide nucleic acid" (PNA) refers to a DNA mimic in which nucleotide bases are attached to a pseudopeptide backbone to increase stability. PNAs, also designated antigene agents, can prevent gene expression by targeting complementary messenger RNA.

The phrases "percent identity" and "% identity", as applied to polynucleotide sequences, refer to the percentage of residue matches between at least two polynucleotide sequences aligned using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps in the sequences being compared in order to optimize alignment between two sequences, and therefore achieve a more meaningful comparison of the two sequences.

Percent identity between polynucleotide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program. This program is part of the LASERGENE software package, a suite of molecular biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G. and Sharp, P.M. (1989) CABIOS 5:151-153 and in Higgins, D.G. et al. (1992) CABIOS 8:189-191. For pairwise alignments of polynucleotide sequences, the default parameters are set as follows: Ktuple=2, gap penalty=5, window=4, and "diagonals saved"=4. The "weighted" residue weight table is

perfectly matched. Permissive conditions for annealing of nucleic acid sequences are routinely determinable and may be consistent among hybridization experiments, whereas wash conditions may be varied among experiments to achieve the desired stringency.

Generally, stringency of hybridization is expressed with reference to the temperature under which the wash step is carried out. Generally, such wash temperatures are selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating T_m and conditions for nucleic acid hybridization is well known and can be found in Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; specifically see volume 2, chapter 9.

High stringency conditions for hybridization between polynucleotides of the present invention include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS, for 1 hour. Alternatively, temperatures of about 65°C, 60°C, or 55°C may be used. SSC concentration may be varied from about 0.2 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, denatured salmon sperm DNA at about 100-200 µg/ml. Useful variations on these conditions will be readily apparent to those skilled in the art. Hybridization, particularly under high stringency conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is strongly indicative of a similar role for the nucleotides and their resultant proteins.

Other parameters, such as temperature, salt concentration, and detergent concentration may be varied to achieve the desired stringency. Denaturants, such as formamide at a concentration of about 35-50% v/v, may also be used under particular circumstances, such as RNA:DNA hybridizations. Appropriate hybridization conditions are routinely determinable by one of ordinary skill in the art.

"Immunogenic" describes the potential for a natural, recombinant, or synthetic peptide, epitope, polypeptide, or protein to induce antibody production in appropriate animals, cells, or cell lines.

"Insertion" or "addition" refers to a change in either a nucleic or amino acid sequence in which at least one nucleotide or residue, respectively, is added to the sequence.

"Labeling" refers to the covalent or noncovalent joining of a polynucleotide, polypeptide, or antibody with a reporter molecule capable of producing a detectable or measurable signal.

"Microarray" is any arrangement of nucleic acids, amino acids, antibodies, etc., on a substrate. The substrate may be a solid support such as beads, glass, paper, nitrocellulose, nylon, or an appropriate membrane.

"Linkers" are short stretches of nucleotide sequence which may be added to a vector or an sptm to create restriction endonuclease sites to facilitate cloning. "Polylinkers" are engineered to incorporate

The phrases "percent identity" and "% identity", as applied to polypeptide sequences, refer to the percentage of residue matches between at least two polypeptide sequences aligned using a standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail above, generally preserve the hydrophobicity and acidity of the substituted residue, thus preserving the structure (and therefore function) of the folded polypeptide.

Percent identity between polypeptide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program (described and referenced above). For pairwise alignments of polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap penalty=3, window=5, and "diagonals saved"=5. The PAM250 matrix is selected as the default residue weight table. As with polynucleotide alignments, the percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polypeptide sequence pairs.

Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise comparison of two polypeptide sequences, one may use the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) with blastp set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Open Gap: 11 and Extension Gap: 1 penalty

Gap x drop-off: 50

Expect: 10

Word Size: 3

Filter: on

Percent identity may be measured over the length of an entire defined polypeptide sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in figures or Sequence Listings, may be used to describe a length over which percentage identity may be measured.

"Post-translational modification" of an SPTM may involve lipidation, glycosylation, phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the art. These processes may occur synthetically or biochemically. Biochemical modifications will vary by cell type depending on the enzymatic milieu and the SPTM.

"Probe" refers to sptm or fragments thereof, which are used to detect identical, allelic or related nucleic acid sequences. Probes are isolated oligonucleotides or polynucleotides attached to a detectable

selected as the default. Percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polynucleotide sequence pairs.

Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at http://www.ncbi.nlm.nih.gov/BLAST/. The BLAST software suite includes various sequence analysis programs including "blastn," that is used to determine alignment between a known polynucleotide sequence and other sequences on a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at http://www.ncbi.nlm.nih.gov/gorf/bl2/. The "BLAST 2 Sequences" tool can be used for both blastn and blastp (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Reward for match: 1

Penalty for mismatch: -2

Open Gap: 5 and Extension Gap: 2 penalties

Gap x drop-off: 50

Expect: 10

Word Size: 11

Filter: on

Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in figures or Sequence Listings, may be used to describe a length over which percentage identity may be measured.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes in nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

polynucleotide fragments. The oligonucleotides and polynucleotide fragments identified by any of the above selection methods are useful in hybridization technologies, for example, as PCR or sequencing primers, microarray elements, or specific probes to identify fully or partially complementary polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

"Purified" refers to molecules, either polynucleotides or polypeptides that are isolated or separated from their natural environment and are at least 60% free, preferably at least 75% free, and most preferably at least 90% free from other compounds with which they are naturally associated.

A "recombinant nucleic acid" is a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two or more otherwise separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques such as those described in Sambrook, supra. The term recombinant includes nucleic acids that have been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence. Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a vaccinia virus, that could be use to vaccinate a mammal wherein the recombinant nucleic acid is expressed, inducing a protective immunological response in the mammal.

"Regulatory element" refers to a nucleic acid sequence from nontranslated regions of a gene, and includes enhancers, promoters, introns, and 3' untranslated regions, which interact with host proteins to carry out or regulate transcription or translation.

"Reporter" molecules are chemical or biochemical moieties used for labeling a nucleic acid, an amino acid, or an antibody. They include radionuclides; enzymes; fluorescent, chemiluminescent, or chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and other moieties known in the art.

An "RNA equivalent," in reference to a DNA sequence, is composed of the same linear sequence of nucleotides as the reference DNA sequence with the exception that all occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

"Sample" is used in its broadest sense. Samples may contain nucleic or amino acids, antibodies, or other materials, and may be derived from any source (e.g., bodily fluids including, but not limited to, saliva, blood, and urine; chromosome(s), organelles, or membranes isolated from a cell; genomic DNA, RNA, or cDNA in solution or bound to a substrate; and cleared cells or tissues or blots or imprints from such cells or tissues).

label or reporter molecule. Typical labels include radioactive isotopes, ligands, chemiluminescent agents, and enzymes. "Primers" are short nucleic acids, usually DNA oligonucleotides, which may be annealed to a target polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR).

Probes and primers as used in the present invention typically comprise at least 15 contiguous nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also be employed, such as probes and primers that comprise at least 20, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the specification, including the figures and Sequence Listing, may be used.

Methods for preparing and using probes and primers are described in the references, for example Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; Ausubel et al.,1987, Current Protocols in Molecular Biology, Greene Publ. Assoc. & Wiley-Intersciences, New York NY; Innis et al., 1990, PCR Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA. PCR primer pairs can be derived from a known sequence, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge MA).

Oligonucleotides for use as primers are selected using software known in the art for such purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to 5,000 nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection programs have incorporated additional features for expanded capabilities. For example, the PrimOU primer selection program (available to the public from the Genome Center at University of Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer selection program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a "mispriming library," in which sequences to avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for microarrays. (The source code for the latter two primer selection programs may also be obtained from their respective sources and modified to meet the user's specific needs.) The PrimeGen program (available to the public from the UK Human Genome Mapping Project Resource Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing selection of primers that hybridize to either the most conserved or least conserved regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both unique and conserved oligonucleotides and

A "variant" of a particular nucleic acid sequence is defined as a nucleic acid sequence having at least 25% sequence identity to the particular nucleic acid sequence over a certain length of one of the nucleic acid sequences using blastn with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of nucleic acids may show, for example, at least 30%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% or even at least 98% or greater sequence identity over a certain defined length. The variant may result in "conservative" amino acid changes which do not affect structural and/or chemical properties. A variant may be described as, for example, an "allelic" (as defined above), "splice," "species," or "polymorphic" variant. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or lack domains that are present in the reference molecule. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides generally will have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

In an alternative, variants of the polynucleotides of the present invention may be generated through recombinant methods. One possible method is a DNA shuffling technique such as MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent Number 5,837,458; Chang, C.-C. et al. (1999) Nat. Biotechnol. 17:793-797; Christians, F.C. et al. (1999) Nat. Biotechnol. 17:259-264; and Crameri, A. et al. (1996) Nat. Biotechnol. 14:315-319) to alter or improve the biological properties of SPTM, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene variants is produced using PCR-mediated recombination of gene fragments. The library is then subjected to selection or screening procedures that identify those gene variants with the desired properties. These preferred variants may then be pooled and further subjected to recursive rounds of DNA shuffling and selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular evolution. For example, fragments of a single gene containing random point mutations may be recombined, screened, and then reshuffled until the desired properties are optimized. Alternatively, fragments of a given gene may be recombined with fragments of homologous genes in the same gene family, either from the same or different species, thereby maximizing the genetic diversity of multiple naturally occurring genes in a directed and controllable manner.

"Specific binding" or "specifically binding" refers to the interaction between a protein or peptide and its agonist, antibody, antagonist, or other binding partner. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide containing epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

"Substitution" refers to the replacement of at least one nucleotide or amino acid by a different nucleotide or amino acid.

"Substrate" refers to any suitable rigid or semi-rigid support including, e.g., membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles or capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

A "transcript image" refers to the collective pattern of gene expression by a particular tissue or cell type under given conditions at a given time.

"Transformation" refers to a process by which exogenous DNA enters a recipient cell. Transformation may occur under natural or artificial conditions using various methods well known in the art. Transformation may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method is selected based on the host cell being transformed.

"Transformants" include stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as cells which transiently express inserted DNA or RNA.

A "transgenic organism," as used herein, is any organism, including but not limited to animals and plants, in which one or more of the cells of the organism contains heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or in vitro fertilization, but rather is directed to the introduction of a recombinant DNA molecule. The transgenic organisms contemplated in accordance with the present invention include bacteria, cyanobacteria, fungi, and plants and animals. The isolated DNA of the present invention can be introduced into the host by methods known in the art, for example infection, transfection, transformation or transconjugation. Techniques for transferring the DNA of the present invention into such organisms are widely known and provided in references such as Sambrook et al. (1989), supra.

VA). Prior to mRNA isolation, cell lines were untreated, treated with a pharmaceutical agent such as 5'-aza-2'-deoxycytidine, treated with an activating agent such as lipopolysaccharide in the case of leukocytic cell lines, or, in the case of endothelial cell lines, subjected to shear stress.

Sequencing of the cDNAs

Methods for DNA sequencing are well known in the art. Conventional enzymatic methods employ the Klenow fragment of DNA polymerase I, SEQUENASE DNA polymerase (U.S. Biochemical Corporation, Cleveland OH), Taq polymerase (PE Biosystems, Foster City CA), thermostable T7 polymerase (Amersham Pharmacia Biotech, Inc. (Amersham Pharmacia Biotech), Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies Inc. (Life Technologies), Gaithersburg MD), to extend the nucleic acid sequence from an oligonucleotide primer annealed to the DNA template of interest. Methods have been developed for the use of both single-stranded and double-stranded templates. Chain termination reaction products may be electrophoresed on urea-polyacrylamide gels and detected either by autoradiography (for radioisotope-labeled nucleotides) or by fluorescence (for fluorophore-labeled nucleotides). Automated methods for mechanized reaction preparation, sequencing, and analysis using fluorescence detection methods have been developed. Machines used to prepare cDNAs for sequencing can include the MICROLAB 2200 liquid transfer system (Hamilton Company (Hamilton), Reno NV), Peltier thermal cycler (PTC200; MJ Research, Inc. (MJ Research), Watertown MA), and ABI CATALYST 800 thermal cycler (PE Biosystems). Sequencing can be carried out using, for example, the ABI 373 or 377 (PE Biosystems) or MEGABACE 1000 (Molecular Dynamics, Inc. (Molecular Dynamics), Sunnyvale CA) DNA sequencing systems, or other automated and manual sequencing systems well known in the art.

The nucleotide sequences of the Sequence Listing have been prepared by current, state-of-the-art, automated methods and, as such, may contain occasional sequencing errors or unidentified nucleotides. Such unidentified nucleotides are designated by an N. These infrequent unidentified bases do not represent a hindrance to practicing the invention for those skilled in the art. Several methods employing standard recombinant techniques may be used to correct errors and complete the missing sequence information. (See, e.g., those described in Ausubel, F.M. et al. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY; and Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY.)

Assembly of cDNA Sequences

Human polynucleotide sequences may be assembled using programs or algorithms well known in the art. Sequences to be assembled are related, wholly or in part, and may be derived from a single or many different transcripts. Assembly of the sequences can be performed using such programs as

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In a particular embodiment, cDNA sequences derived from human tissues and cell lines were aligned based on nucleotide sequence identity and assembled into "consensus" or "template" sequences which are designated by the template identification numbers (template IDs) in column 2 of Table 1. The sequence identification numbers (SEQ ID NO:s) corresponding to the template IDs are shown in column 1. Segments of the template sequences are defined by the "start" and "stop" nucleotide positions listed in columns 3 and 4. These segments, when translated in the reading frames indicated in column 5, have similarity to signal peptide (SP) or transmembrane (TM) domain consensus sequences, as indicated in column 6.

The invention incorporates the nucleic acid sequences of these templates as disclosed in the Sequence Listing and the use of these sequences in the diagnosis and treatment of disease states characterized by defects in cell signaling. The invention further utilizes these sequences in hybridization and amplification technologies, and in particular, in technologies which assess gene expression patterns correlated with specific cells or tissues and their responses in vivo or in vitro to pharmaceutical agents, toxins, and other treatments. In this manner, the sequences of the present invention are used to develop a transcript image for a particular cell or tissue.

Derivation of Nucleic Acid Sequences

cDNA was isolated from libraries constructed using RNA derived from normal and diseased human tissues and cell lines. The human tissues and cell lines used for cDNA library construction were selected from a broad range of sources to provide a diverse population of cDNAs representative of gene transcription throughout the human body. Descriptions of the human tissues and cell lines used for cDNA library construction are provided in the LIFESEQ database (Incyte Genomics, Inc. (Incyte), Palo Alto CA). Human tissues were broadly selected from, for example, cardiovascular, dermatologic, endocrine, gastrointestinal, hematopoietic/immune system, musculoskeletal, neural, reproductive, and urologic sources.

Cell lines used for cDNA library construction were derived from, for example, leukemic cells, teratocarcinomas, neuroepitheliomas, cervical carcinoma, lung fibroblasts, and endothelial cells. Such cell lines include, for example, THP-1, Jurkat, HUVEC, hNT2, WI38, HeLa, and other cell lines commonly used and available from public depositories (American Type Culture Collection, Manassas

Computer programs known to those of skill in the art for performing computer-assisted searches for amino acid and nucleic acid sequence similarity, include, for example, Basic Local Alignment Search Tool (BLAST; Altschul, S.F. (1993) J. Mol. Evol. 36:290-300; Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410). BLAST is especially useful in determining exact matches and comparing two sequence fragments of arbitrary but equal lengths, whose alignment is locally maximal and for which the alignment score meets or exceeds a threshold or cutoff score set by the user (Karlin, S. et al. (1988) Proc. Natl. Acad. Sci. USA 85:841-845). Using an appropriate search tool (e.g., BLAST or HMM), GenBank, SwissProt, BLOCKS, PFAM and other databases may be searched for sequences containing regions of homology to a query sptm or SPTM of the present invention.

Other approaches to the identification, assembly, storage, and display of nucleotide and polypeptide sequences are provided in "Relational Database for Storing Biomolecule Information," U.S.S.N. 08/947,845, filed October 9, 1997; "Project-Based Full-Length Biomolecular Sequence Database," U.S.S.N. 08/811,758, filed March 6, 1997; and "Relational Database and System for Storing Information Relating to Biomolecular Sequences," U.S.S.N. 09/034,807, filed March 4, 1998, all of which are incorporated by reference herein in their entirety.

Protein hierarchies can be assigned to the putative encoded polypeptide based on, e.g., motif, BLAST, or biological analysis. Methods for assigning these hierarchies are described, for example, in "Database System Employing Protein Function Hierarchies for Viewing Biomolecular Sequence Data," U.S.S.N. 08/812,290, filed March 6, 1997, incorporated herein by reference.

Human Secretory Sequences

The sptm of the present invention may be used for a variety of diagnostic and therapeutic purposes. For example, an sptm may be used to diagnose a particular condition, disease, or disorder associated with cell signaling. Such conditions, diseases, and disorders include, but are not limited to, a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, a cancer of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; an immune system disorder such as such as inflammation, actinic keratosis, acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, arteriosclerosis, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, bronchitis, bursitis, cholecystitis, cirrhosis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, erythroblastosis fetalis,

PHRAP (Phils Revised Assembly Program) and the GELVIEW fragment assembly system (GCG), or other methods known in the art.

Alternatively, cDNA sequences are used as "component" sequences that are assembled into "template" or "consensus" sequences as follows. Sequence chromatograms are processed, verified, and quality scores are obtained using PHRED. Raw sequences are edited using an editing pathway known as Block 1 (See, e.g., the LIFESEQ Assembled User Guide, Incyte Genomics, Palo Alto, CA). A series of BLAST comparisons is performed and low-information segments and repetitive elements (e.g., dinucleotide repeats, Alu repeats, etc.) are replaced by "n's", or masked, to prevent spurious matches. Mitochondrial and ribosomal RNA sequences are also removed. The processed sequences are then loaded into a relational database management system (RDMS) which assigns edited sequences to existing templates, if available. When additional sequences are added into the RDMS, a process is initiated which modifies existing templates or creates new templates from works in progress (i.e., nonfinal assembled sequences) containing queued sequences or the sequences themselves. After the new sequences have been assigned to templates, the templates can be merged into bins. If multiple templates exist in one bin, the bin can be split and the templates reannotated.

Once gene bins have been generated based upon sequence alignments, bins are "clone joined" based upon clone information. Clone joining occurs when the 5' sequence of one clone is present in one bin and the 3' sequence from the same clone is present in a different bin, indicating that the two bins should be merged into a single bin. Only bins which share at least two different clones are merged.

A resultant template sequence may contain either a partial or a full length open reading frame, or all or part of a genetic regulatory element. This variation is due in part to the fact that the full length cDNAs of many genes are several hundred, and sometimes several thousand, bases in length. With current technology, cDNAs comprising the coding regions of large genes cannot be cloned because of vector limitations, incomplete reverse transcription of the mRNA, or incomplete "second strand" synthesis. Template sequences may be extended to include additional contiguous sequences derived from the parent RNA transcript using a variety of methods known to those of skill in the art. Extension may thus be used to achieve the full length coding sequence of a gene.

Analysis of the cDNA Sequences

The cDNA sequences are analyzed using a variety of programs and algorithms which are well known in the art. (See, e.g., Ausubel, 1997, supra, Chapter 7.7; Meyers, R.A. (Ed.) (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853; and Table 4.) These analyses comprise both reading frame determinations, e.g., based on triplet codon periodicity for particular organisms (Fickett, J.W. (1982) Nucleic Acids Res. 10:5303-5318); analyses of potential start and stop codons; and homology searches.

of analysis is useful, for example, to assess the relative levels of sptm expression in fully or partially differentiated cells or tissues, to determine if changes in sptm expression levels are correlated with the development or progression of specific disease states, and to assess the response of a cell or tissue to a specific therapy, for example, in pharmacological or toxicological studies. Methods for the analysis of sptm expression are based on hybridization and amplification technologies and include membrane-based procedures such as northern blot analysis, high-throughput procedures that utilize, for example, microarrays, and PCR-based procedures.

Hybridization and Genetic Analysis

The sptm, their fragments, or complementary sequences, may be used to identify the presence of and/or to determine the degree of similarity between two (or more) nucleic acid sequences. The sptm may be hybridized to naturally occurring or recombinant nucleic acid sequences under appropriately selected temperatures and salt concentrations. Hybridization with a probe based on the nucleic acid sequence of at least one of the sptm allows for the detection of nucleic acid sequences, including genomic sequences, which are identical or related to the sptm of the Sequence Listing. Probes may be selected from non-conserved or unique regions of at least one of the polynucleotides of SEQ ID NO:1-63 and tested for their ability to identify or amplify the target nucleic acid sequence using standard protocols.

Polynucleotide sequences that are capable of hybridizing, in particular, to those shown in SEQ ID NO:1-63 and fragments thereof, can be identified using various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) Methods Enzymol. 152:399-407; Kimmel, A.R. (1987) Methods Enzymol. 152:507-511.) Hybridization conditions are discussed in "Definitions."

A probe for use in Southern or northern hybridization may be derived from a fragment of an sptm sequence, or its complement, that is up to several hundred nucleotides in length and is either single-stranded or double-stranded. Such probes may be hybridized in solution to biological materials such as plasmids, bacterial, yeast, or human artificial chromosomes, cleared or sectioned tissues, or to artificial substrates containing sptm. Microarrays are particularly suitable for identifying the presence of and detecting the level of expression for multiple genes of interest by examining gene expression correlated with, e.g., various stages of development, treatment with a drug or compound, or disease progression. An array analogous to a dot or slot blot may be used to arrange and link polynucleotides to the surface of a substrate using one or more of the following: mechanical (vacuum), chemical, thermal, or UV bonding procedures. Such an array may contain any number of sptm and may be produced by hand or by using available devices, materials, and machines.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci.

erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, paroxysmal nocturnal hemoglobinuria, hepatitis, hypereosinophilia, irritable bowel syndrome, episodic lymphopenia with lymphocytotoxins, mixed connective tissue disease (MCTD), multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, myelofibrosis, osteoarthritis, osteoporosis, pancreatitis, polycythemia vera, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, primary thrombocythemia, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, trauma, and hematopoietic cancer including lymphoma, leukemia, and myeloma; and a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorder of the central nervous system, cerebral palsy, a neuroskeletal disorder, an autonomic nervous system disorder, a cranial nerve disorder, a spinal cord disease, muscular dystrophy and other neuromuscular disorder, a peripheral nervous system disorder, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathy, myasthenia gravis, periodic paralysis, a mental disorder including mood, anxiety, and schizophrenic disorder, seasonal affective disorder (SAD), akathesia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, and Tourette's disorder. The sptm can be used to detect the presence of, or to quantify the amount of, an sptm-related polynucleotide in a sample. This information is then compared to information obtained from appropriate reference samples, and a diagnosis is established. Alternatively, a polynucleotide complementary to a given sptm can inhibit or inactivate a therapeutically relevant gene related to the sptm.

Analysis of sptm Expression Patterns

The expression of sptm may be routinely assessed by hybridization-based methods to determine, for example, the tissue-specificity, disease-specificity, or developmental stage-specificity of sptm expression. For example, the level of expression of sptm may be compared among different cell types or tissues, among diseased and normal cell types or tissues, among cell types or tissues at different developmental stages, or among cell types or tissues undergoing various treatments. This type

linkage maps can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) World Wide Web site.

In another embodiment of the invention, sptm sequences may be used to generate hybridization probes useful in chromosomal mapping of naturally occurring genomic sequences. Either coding or noncoding sequences of sptm may be used, and in some instances, noncoding sequences may be preferable over coding sequences. For example, conservation of an sptm coding sequence among members of a multi-gene family may potentially cause undesired cross hybridization during chromosomal mapping. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical chromosome mapping techniques and genetic map data. (See, e.g., Meyers, supra, pp. 965-968.) Correlation between the location of sptm on a physical chromosomal map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder. The sptm sequences may also be used to detect polymorphisms that are genetically linked to the inheritance of a particular condition, disease, or disorder.

In situ hybridization of chromosomal preparations and genetic mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending existing genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the number or arm of the corresponding human chromosome is not known. These new marker sequences can be mapped to human chromosomes and may provide valuable information to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once a disease or syndrome has been crudely correlated by genetic linkage with a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequences of the subject invention may also be used to detect differences in chromosomal architecture due to translocation, inversion, etc., among normal, carrier, or affected individuals.

Once a disease-associated gene is mapped to a chromosomal region, the gene must be cloned in order to identify mutations or other alterations (e.g., translocations or inversions) that may be correlated with disease. This process requires a physical map of the chromosomal region containing the disease-gene of interest along with associated markers. A physical map is necessary for determining the

USA 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. USA 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.)

Probes may be labeled by either PCR or enzymatic techniques using a variety of commercially available reporter molecules. For example, commercial kits are available for radioactive and chemiluminescent labeling (Amersham Pharmacia Biotech) and for alkaline phosphatase labeling (Life Technologies). Alternatively, sptm may be cloned into commercially available vectors for the production of RNA probes. Such probes may be transcribed in the presence of at least one labeled nucleotide (e.g., ^{32}P-ATP, Amersham Pharmacia Biotech).

Additionally the polynucleotides of SEQ ID NO:1-63 or suitable fragments thereof can be used to isolate full length cDNA sequences utilizing hybridization and/or amplification procedures well known in the art, e.g., cDNA library screening, PCR amplification, etc. The molecular cloning of such full length cDNA sequences may employ the method of cDNA library screening with probes using the hybridization, stringency, washing, and probing strategies described above and in Ausubel, supra, Chapters 3, 5, and 6. These procedures may also be employed with genomic libraries to isolate genomic sequences of sptm in order to analyze, e.g., regulatory elements.

Genetic Mapping

Gene identification and mapping are important in the investigation and treatment of almost all conditions, diseases, and disorders. Cancer, cardiovascular disease, Alzheimer's disease, arthritis, diabetes, and mental illnesses are of particular interest. Each of these conditions is more complex than the single gene defects of sickle cell anemia or cystic fibrosis, with select groups of genes being predictive of predisposition for a particular condition, disease, or disorder. For example, cardiovascular disease may result from malfunctioning receptor molecules that fail to clear cholesterol from the bloodstream, and diabetes may result when a particular individual's immune system is activated by an infection and attacks the insulin-producing cells of the pancreas. In some studies, Alzheimer's disease has been linked to a gene on chromosome 21; other studies predict a different gene and location. Mapping of disease genes is a complex and reiterative process and generally proceeds from genetic linkage analysis to physical mapping.

As a condition is noted among members of a family, a genetic linkage map traces parts of chromosomes that are inherited in the same pattern as the condition. Statistics link the inheritance of particular conditions to particular regions of chromosomes, as defined by RFLP or other markers. (See, for example, Lander, E. S. and Botstein, D. (1986) Proc. Natl. Acad. Sci. USA 83:7353-7357.) Occasionally, genetic markers and their locations are known from previous studies. More often, however, the markers are simply stretches of DNA that differ among individuals. Examples of genetic

primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, an individual can be identified through a unique set of DNA sequences. Once a unique ID database is established for an individual, positive identification of that individual can be made from extremely small tissue samples.

In a particular aspect, oligonucleotide primers derived from the sptm of the invention may be used to detect single nucleotide polymorphisms (SNPs). SNPs are substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic disease in humans. Methods of SNP detection include, but are not limited to, single-stranded conformation polymorphism (SSCP) and fluorescent SSCP (fSSCP) methods. In SSCP, oligonucleotide primers derived from sptm are used to amplify DNA using the polymerase chain reaction (PCR). The DNA may be derived, for example, from diseased or normal tissue, biopsy samples, bodily fluids, and the like. SNPs in the DNA cause differences in the secondary and tertiary structures of PCR products in single-stranded form, and these differences are detectable using gel electrophoresis in non-denaturing gels. In fSCCP, the oligonucleotide primers are fluorescently labeled, which allows detection of the amplimers in high-throughput equipment such as DNA sequencing machines. Additionally, sequence database analysis methods, termed in silico SNP (isSNP), are capable of identifying polymorphisms by comparing the sequences of individual overlapping DNA fragments which assemble into a common consensus sequence. These computer-based methods filter out sequence variations due to laboratory preparation of DNA and sequencing errors using statistical models and automated analyses of DNA sequence chromatograms. In the alternative, SNPs may be detected and characterized by mass spectrometry using, for example, the high throughput MASSARRAY system (Sequenom, Inc., San Diego CA).

DNA-based identification techniques are critical in forensic technology. DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, etc., can be amplified using, e.g., PCR, to identify individuals. (See, e.g., Erlich, H. (1992) PCR Technology, Freeman and Co., New York, NY). Similarly, polynucleotides of the present invention can be used as polymorphic markers.

There is also a need for reagents capable of identifying the source of a particular tissue. Appropriate reagents can comprise, for example, DNA probes or primers prepared from the sequences of the present invention that are specific for particular tissues. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

The polynucleotides of the present invention can also be used as molecular weight markers on nucleic acid gels or Southern blots, as diagnostic probes for the presence of a specific mRNA in a particular cell type, in the creation of subtracted cDNA libraries which aid in the discovery of novel

nucleotide sequence of and order of marker genes on a particular chromosomal region. Physical mapping techniques are well known in the art and require the generation of overlapping sets of cloned DNA fragments from a particular organelle, chromosome, or genome. These clones are analyzed to reconstruct and catalog their order. Once the position of a marker is determined, the DNA from that region is obtained by consulting the catalog and selecting clones from that region. The gene of interest is located through positional cloning techniques using hybridization or similar methods.

Diagnostic Uses

The sptm of the present invention may be used to design probes useful in diagnostic assays. Such assays, well known to those skilled in the art, may be used to detect or confirm conditions, disorders, or diseases associated with abnormal levels of sptm expression. Labeled probes developed from sptm sequences are added to a sample under hybridizing conditions of desired stringency. In some instances, sptm, or fragments or oligonucleotides derived from sptm, may be used as primers in amplification steps prior to hybridization. The amount of hybridization complex formed is quantified and compared with standards for that cell or tissue. If sptm expression varies significantly from the standard, the assay indicates the presence of the condition, disorder, or disease. Qualitative or quantitative diagnostic methods may include northern, dot blot, or other membrane or dip-stick based technologies or multiple-sample format technologies such as PCR, enzyme-linked immunosorbent assay (ELISA)-like, pin, or chip-based assays.

The probes described above may also be used to monitor the progress of conditions, disorders, or diseases associated with abnormal levels of sptm expression, or to evaluate the efficacy of a particular therapeutic treatment. The candidate probe may be identified from the sptm that are specific to a given human tissue and have not been observed in GenBank or other genome databases. Such a probe may be used in animal studies, preclinical tests, clinical trials, or in monitoring the treatment of an individual patient. In a typical process, standard expression is established by methods well known in the art for use as a basis of comparison, samples from patients affected by the disorder or disease are combined with the probe to evaluate any deviation from the standard profile, and a therapeutic agent is administered and effects are monitored to generate a treatment profile. Efficacy is evaluated by determining whether the expression progresses toward or returns to the standard normal pattern. Treatment profiles may be generated over a period of several days or several months. Statistical methods well known to those skilled in the art may be use to determine the significance of such therapeutic agents.

The polynucleotides are also useful for identifying individuals from minute biological samples, for example, by matching the RFLP pattern of a sample's DNA to that of an individual's DNA. The polynucleotides of the present invention can also be used to determine the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be used to prepare PCR

bound molecule. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a ligand or fragment thereof, a natural substrate, or a structural or functional mimetic. (See, Coligan et al., (1991) Current Protocols in Immunology 1(2): Chapter 5.) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or to at least a fragment of the receptor, e.g., the active site. In either case, the molecule can be rationally designed using known techniques. Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or E. coli. Cells expressing the polypeptide or cell membrane fractions which contain the expressed polypeptide are then contacted with a test compound and binding, stimulation, or inhibition of activity of either the polypeptide or the molecule is analyzed.

An assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a fluorophore, radioisotope, enzyme conjugate, or other detectable label. Alternatively, the assay may assess binding in the presence of a labeled competitor.

Additionally, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

Preferably, an ELISA assay using, e.g., a monoclonal or polyclonal antibody, can measure polypeptide level in a sample. The antibody can measure polypeptide level by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

All of the above assays can be used in a diagnostic or prognostic context. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptide from suitably manipulated cells or tissues.

Transcript Imaging and Toxicological Testing

Another embodiment relates to the use of sptm to develop a transcript image of a tissue or cell type. A transcript image represents the global pattern of gene expression by a particular tissue or cell type. Global gene expression patterns are analyzed by quantifying the number of expressed genes and their relative abundance under given conditions and at a given time. (See Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, expressly incorporated by reference herein.) Thus a transcript image may be generated by hybridizing the polynucleotides of the

polynucleotides, in selection and synthesis of oligomers for attachment to an array or other support, and as an antigen to elicit an immune response.

Disease Model Systems Using SPTM

The polynucleotides encoding SPTM or their mammalian homologs may be "knocked out" in an animal model system using homologous recombination in embryonic stem (ES) cells. Such techniques are well known in the art and are useful for the generation of animal models of human disease. (See, e.g., U.S. Patent Number 5,175,383 and U.S. Patent Number 5,767,337.) For example, mouse ES cells, such as the mouse 129/SvJ cell line, are derived from the early mouse embryo and grown in culture. The ES cells are transformed with a vector containing the gene of interest disrupted by a marker gene, e.g., the neomycin phosphotransferase gene (neo; Capecchi, M.R. (1989) Science 244:1288-1292). The vector integrates into the corresponding region of the host genome by homologous recombination. Alternatively, homologous recombination takes place using the Cre-loxP system to knockout a gene of interest in a tissue- or developmental stage-specific manner (Marth, J.D. (1996) Clin. Invest. 97:1999-2002; Wagner, K.U. et al. (1997) Nucleic Acids Res. 25:4323-4330). Transformed ES cells are identified and microinjected into mouse cell blastocysts such as those from the C57BL/6 mouse strain. The blastocysts are surgically transferred to pseudopregnant dams, and the resulting chimeric progeny are genotyped and bred to produce heterozygous or homozygous strains. Transgenic animals thus generated may be tested with potential therapeutic or toxic agents.

Polynucleotides encoding SPTM may also be manipulated in vitro in ES cells derived from human blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al. (1998) Science 282:1145-1147).

Polynucleotides encoding SPTM can also be used to create "knockin" humanized animals (pigs) or transgenic animals (mice or rats) to model human disease. With knockin technology, a region of sptm is injected into animal ES cells, and the injected sequence integrates into the animal cell genome. Transformed cells are injected into blastulae, and the blastulae are implanted as described above. Transgenic progeny or inbred lines are studied and treated with potential pharmaceutical agents to obtain information on treatment of a human disease. Alternatively, a mammal inbred to overexpress sptm, resulting, e.g., in the secretion of SPTM in its milk, may also serve as a convenient source of that protein (Janne, J. et al. (1998) Biotechnol. Annu. Rev. 4:55-74).

Screening Assays

SPTM encoded by polynucleotides of the present invention may be used to screen for molecules that bind to or are bound by the encoded polypeptides. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit (antagonist), or decrease activity of the polypeptide or the

Another particular embodiment relates to the use of SPTM encoded by polynucleotides of the present invention to analyze the proteome of a tissue or cell type. The term proteome refers to the global pattern of protein expression in a particular tissue or cell type. Each protein component of a proteome can be subjected individually to further analysis. Proteome expression patterns, or profiles, are analyzed by quantifying the number of expressed proteins and their relative abundance under given conditions and at a given time. A profile of a cell's proteome may thus be generated by separating and analyzing the polypeptides of a particular tissue or cell type. In one embodiment, the separation is achieved using two-dimensional gel electrophoresis, in which proteins from a sample are separated by isoelectric focusing in the first dimension, and then according to molecular weight by sodium dodecyl sulfate slab gel electrophoresis in the second dimension (Steiner and Anderson, supra). The proteins are visualized in the gel as discrete and uniquely positioned spots, typically by staining the gel with an agent such as Coomassie Blue or silver or fluorescent stains. The optical density of each protein spot is generally proportional to the level of the protein in the sample. The optical densities of equivalently positioned protein spots from different samples, for example, from biological samples either treated or untreated with a test compound or therapeutic agent, are compared to identify any changes in protein spot density related to the treatment. The proteins in the spots are partially sequenced using, for example, standard methods employing chemical or enzymatic cleavage followed by mass spectrometry. The identity of the protein in a spot may be determined by comparing its partial sequence, preferably of at least 5 contiguous amino acid residues, to the polypeptide sequences of the present invention. In some cases, further sequence data may be obtained for definitive protein identification.

A proteomic profile may also be generated using antibodies specific for SPTM to quantify the levels of SPTM expression. In one embodiment, the antibodies are used as elements on a microarray, and protein expression levels are quantified by exposing the microarray to the sample and detecting the levels of protein bound to each array element (Lueking, A. et al. (1999) Anal. Biochem. 270:103-11; Mendoze, L. G. et al. (1999) Biotechniques 27:778-88). Detection may be performed by a variety of methods known in the art, for example, by reacting the proteins in the sample with a thiol- or amino-reactive fluorescent compound and detecting the amount of fluorescence bound at each array element.

Toxicant signatures at the proteome level are also useful for toxicological screening, and should be analyzed in parallel with toxicant signatures at the transcript level. There is a poor correlation between transcript and protein abundances for some proteins in some tissues (Anderson, N. L. and Seilhamer, J. (1997) Electrophoresis 18:533-537), so proteome toxicant signatures may be useful in the analysis of compounds which do not significantly affect the transcript image, but which alter the proteomic profile. In addition, the analysis of transcripts in body fluids is difficult, due to rapid degradation of mRNA, so proteomic profiling may be more reliable and informative in such cases.

present invention or their complements to the totality of transcripts or reverse transcripts of a particular tissue or cell type. In one embodiment, the hybridization takes place in high-throughput format, wherein the polynucleotides of the present invention or their complements comprise a subset of a plurality of elements on a microarray. The resultant transcript image would provide a profile of gene activity pertaining to cell signaling.

Transcript images which profile sptm expression may be generated using transcripts isolated from tissues, cell lines, biopsies, or other biological samples. The transcript image may thus reflect sptm expression in vivo, as in the case of a tissue or biopsy sample, or in vitro, as in the case of a cell line.

Transcript images which profile sptm expression may also be used in conjunction with in vitro model systems and preclinical evaluation of pharmaceuticals, as well as toxicological testing of industrial and naturally-occurring environmental compounds. All compounds induce characteristic gene expression patterns, frequently termed molecular fingerprints or toxicant signatures, which are indicative of mechanisms of action and toxicity (Nuwaysir, E. F. et al. (1999) Mol. Carcinog. 24:153-159; Steiner, S. and Anderson, N. L. (2000) Toxicol. Lett. 112-113:467-71, expressly incorporated by reference herein). If a test compound has a signature similar to that of a compound with known toxicity, it is likely to share those toxic properties. These fingerprints or signatures are most useful and refined when they contain expression information from a large number of genes and gene families. Ideally, a genome-wide measurement of expression provides the highest quality signature. Even genes whose expression is not altered by any tested compounds are important as well, as the levels of expression of these genes are used to normalize the rest of the expression data. The normalization procedure is useful for comparison of expression data after treatment with different compounds. While the assignment of gene function to elements of a toxicant signature aids in interpretation of toxicity mechanisms, knowledge of gene function is not necessary for the statistical matching of signatures which leads to prediction of toxicity. (See, for example, Press Release 00-02 from the National Institute of Environmental Health Sciences, released February 29, 2000, available at http://www.niehs.nih.gov/oc/news/toxchip.htm.) Therefore, it is important and desirable in toxicological screening using toxicant signatures to include all expressed gene sequences.

In one embodiment, the toxicity of a test compound is assessed by treating a biological sample containing nucleic acids with the test compound. Nucleic acids that are expressed in the treated biological sample are hybridized with one or more probes specific to the polynucleotides of the present invention, so that transcript levels corresponding to the polynucleotides of the present invention may be quantified. The transcript levels in the treated biological sample are compared with levels in an untreated biological sample. Differences in the transcript levels between the two samples are indicative of a toxic response caused by the test compound in the treated sample.

al. (1997) Biochem. Mol. Med. 62(1):11-22.) An antisense sequence is a polynucleotide sequence capable of specifically hybridizing to at least a portion of the target sequence. Antisense sequences bind to cellular mRNA and/or genomic DNA, affecting translation and/or transcription. Antisense sequences can be DNA, RNA, or nucleic acid mimics and analogs. (See, e.g., Rossi, J.J. et al. (1991) Antisense Res. Dev. 1(3):285-288; Lee, R. et al. (1998) Biochemistry 37(3):900-1010; Pardridge, W.M. et al. (1995) Proc. Natl. Acad. Sci. USA 92(12):5592-5596; and Nielsen, P. E. and Haaima, G. (1997) Chem. Soc. Rev. 96:73-78.) Typically, the binding which results in modulation of expression occurs through hybridization or binding of complementary base pairs. Antisense sequences can also bind to DNA duplexes through specific interactions in the major groove of the double helix.

The polynucleotides of the present invention and fragments thereof can be used as antisense sequences to modify the expression of the polypeptide encoded by sptm. The antisense sequences can be produced ex vivo, such as by using any of the ABI nucleic acid synthesizer series (PE Biosystems) or other automated systems known in the art. Antisense sequences can also be produced biologically, such as by transforming an appropriate host cell with an expression vector containing the sequence of interest. (See, e.g., Agrawal, supra.)

In therapeutic use, any gene delivery system suitable for introduction of the antisense sequences into appropriate target cells can be used. Antisense sequences can be delivered intracellularly in the form of an expression plasmid which, upon transcription, produces a sequence complementary to at least a portion of the cellular sequence encoding the target protein. (See, e.g., Slater, J.E., et al. (1998) J. Allergy Clin. Immunol. 102(3):469-475; and Scanlon, K.J., et al. (1995) 9(13):1288-1296.) Antisense sequences can also be introduced intracellularly through the use of viral vectors, such as retrovirus and adeno-associated virus vectors. (See, e.g., Miller, A.D. (1990) Blood 76:271; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY; Uckert, W. and W. Walther (1994) Pharmacol. Ther. 63(3):323-347.) Other gene delivery mechanisms include liposome-derived systems, artificial viral envelopes, and other systems known in the art. (See, e.g., Rossi, J.J. (1995) Br. Med. Bull. 51(1):217-225; Boado, R.J. et al. (1998) J. Pharm. Sci. 87(11):1308-1315; and Morris, M.C. et al. (1997) Nucleic Acids Res. 25(14):2730-2736.)

Expression

In order to express a biologically active SPTM, the nucleotide sequences encoding SPTM or fragments thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding SPTM and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins that are expressed in the treated biological sample are separated so that the amount of each protein can be quantified. The amount of each protein is compared to the amount of the corresponding protein in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample. Individual proteins are identified by sequencing the amino acid residues of the individual proteins and comparing these partial sequences to the SPTM encoded by polynucleotides of the present invention.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins from the biological sample are incubated with antibodies specific to the SPTM encoded by polynucleotides of the present invention. The amount of protein recognized by the antibodies is quantified. The amount of protein in the treated biological sample is compared with the amount in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample.

Transcript images may be used to profile sptm expression in distinct tissue types. This process can be used to determine cell signaling activity in a particular tissue type relative to this activity in a different tissue type. Transcript images may be used to generate a profile of sptm expression characteristic of diseased tissue. Transcript images of tissues before and after treatment may be used for diagnostic purposes, to monitor the progression of disease, and to monitor the efficacy of drug treatments for diseases which affect cell signaling activity.

Transcript images of cell lines can be used to assess cell signaling activity and/or to identify cell lines that lack or misregulate this activity. Such cell lines may then be treated with pharmaceutical agents, and a transcript image following treatment may indicate the efficacy of these agents in restoring desired levels of this activity. A similar approach may be used to assess the toxicity of pharmaceutical agents as reflected by undesirable changes in cell signaling activity. Candidate pharmaceutical agents may be evaluated by comparing their associated transcript images with those of pharmaceutical agents of known effectiveness.

Antisense Molecules

The polynucleotides of the present invention are useful in antisense technology. Antisense technology or therapy relies on the modulation of expression of a target protein through the specific binding of an antisense sequence to a target sequence encoding the target protein or directing its expression. (See, e.g., Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press Inc., Totawa NJ; Alama, A. et al. (1997) Pharmacol. Res. 36(3):171-178; Crooke, S.T. (1997) Adv. Pharmacol. 40:1-49; Sharma, H.W. and R. Narayanan (1995) Bioessays 17(12):1055-1063; and Lavrosky, Y. et

immunodeficiency (SCID)-X1 disease characterized by X-linked inheritance (Cavazzana-Calvo, M. et al. (2000) Science 288:669-672), severe combined immunodeficiency syndrome associated with an inherited adenosine deaminase (ADA) deficiency (Blaese, R.M. et al. (1995) Science 270:475-480; Bordignon, C. et al. (1995) Science 270:470-475), cystic fibrosis (Zabner, J. et al. (1993) Cell 75:207-216; Crystal, R.G. et al. (1995) Hum. Gene Therapy 6:643-666; Crystal, R.G. et al. (1995) Hum. Gene Therapy 6:667-703), thalassemias, familial hypercholesterolemia, and hemophilia resulting from Factor VIII or Factor IX deficiencies (Crystal, R.G. (1995) Science 270:404-410; Verma, I.M. and Somia, N. (1997) Nature 389:239-242)), (ii) express a conditionally lethal gene product (e.g., in the case of cancers which result from unregulated cell proliferation), or (iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988) Nature 335:395-396; Poeschla, E. et al. (1996) Proc. Natl. Acad. Sci. USA. 93:11395-11399), hepatitis B or C virus (HBV, HCV); fungal parasites, such as Candida albicans and Paracoccidioides brasiliensis; and protozoan parasites such as Plasmodium falciparum and Trypanosoma cruzi). In the case where a genetic deficiency in sptm expression or regulation causes disease, the expression of sptm from an appropriate population of transduced cells may alleviate the clinical manifestations caused by the genetic deficiency.

In a further embodiment of the invention, diseases or disorders caused by deficiencies in sptm are treated by constructing mammalian expression vectors comprising sptm and introducing these vectors by mechanical means into sptm-deficient cells. Mechanical transfer technologies for use with cells in vivo or ex vitro include (i) direct DNA microinjection into individual cells, (ii) ballistic gold particle delivery, (iii) liposome-mediated transfection, (iv) receptor-mediated gene transfer, and (v) the use of DNA transposons (Morgan, R.A. and Anderson, W.F. (1993) Annu. Rev. Biochem. 62:191-217; Ivics, Z. (1997) Cell 91:501-510; Boulay, J-L. and Récipon, H. (1998) Curr. Opin. Biotechnol. 9:445-450).

Expression vectors that may be effective for the expression of sptm include, but are not limited to, the PCDNA 3.1, EPITAG, PRCCMV2, PREP, PVAX vectors (Invitrogen, Carlsbad CA), PCMV-SCRIPT, PCMV-TAG, PEGSH/PERV (Stratagene, La Jolla CA), and PTET-OFF, PTET-ON, PTRE2, PTRE2-LUC, PTK-HYG (Clontech, Palo Alto CA). The sptm of the invention may be expressed using (i) a constitutively active promoter, (e.g., from cytomegalovirus (CMV), Rous sarcoma virus (RSV), SV40 virus, thymidine kinase (TK), or β-actin genes), (ii) an inducible promoter (e.g., the tetracycline-regulated promoter (Gossen, M. and Bujard, H. (1992) Proc. Natl. Acad. Sci. U.S.A. 89:5547-5551; Gossen, M. et al., (1995) Science 268:1766-1769; Rossi, F.M.V. and Blau, H.M. (1998) Curr. Opin. Biotechnol. 9:451-456), commercially available in the T-REX plasmid (Invitrogen); the ecdysone-inducible promoter (available in the plasmids PVGRXR and PIND; Invitrogen); the FK506/rapamycin inducible promoter; or the RU486/mifepristone inducible promoter

techniques, and in vivo genetic recombination. (See, e.g., Sambrook, supra, Chapters 4, 8, 16, and 17; and Ausubel, supra, Chapters 9, 10, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences encoding SPTM. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal (mammalian) cell systems. (See, e.g., Sambrook, supra; Ausubel, 1995, supra, Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509; Bitter, G.A. et al. (1987) Methods Enzymol. 153:516-544; Scorer, C.A. et al. (1994) Bio/Technology 12:181-184; Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945; Takamatsu, N. (1987) EMBO J. 6:307-311; Coruzzi, G. et al. (1984) EMBO J. 3:1671-1680; Broglie, R. et al. (1984) Science 224:838-843; Winter, J. et al. (1991) Results Probl. Cell Differ. 17:85-105; The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196; Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659; and Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.) Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. (See, e.g., Di Nicola, M. et al. (1998) Cancer Gen. Ther. 5(6):350-356; Yu, M. et al., (1993) Proc. Natl. Acad. Sci. USA 90(13):6340-6344; Buller, R.M. et al. (1985) Nature 317(6040):813-815; McGregor, D.P. et al. (1994) Mol. Immunol. 31(3):219-226; and Verma, I.M. and N. Somia (1997) Nature 389:239-242.) The invention is not limited by the host cell employed.

For long term production of recombinant proteins in mammalian systems, stable expression of SPTM in cell lines is preferred. For example, sequences encoding SPTM can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Any number of selection systems may be used to recover transformed cell lines. (See, e.g., Wigler, M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.; Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14; Hartman, S.C. and R.C.Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:8047-8051; Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

Therapeutic Uses of sptm

The polynucleotides encoding SPTM may be used for somatic or germline gene therapy. Gene therapy may be performed to (i) correct a genetic deficiency (e.g., in the cases of severe combined

Number 5,707,618 to Armentano ("Adenovirus vectors for gene therapy"), hereby incorporated by reference. For adenoviral vectors, see also Antinozzi, P.A. et al. (1999) Annu. Rev. Nutr. 19:511-544 and Verma, I.M. and Somia, N. (1997) Nature 18:389:239-242, both incorporated by reference herein.

In another alternative, a herpes-based, gene therapy delivery system is used to deliver sptm to target cells which have one or more genetic abnormalities with respect to the expression of sptm. The use of herpes simplex virus (HSV)-based vectors may be especially valuable for introducing sptm to cells of the central nervous system, for which HSV has a tropism. The construction and packaging of herpes-based vectors are well known to those with ordinary skill in the art. A replication-competent herpes simplex virus (HSV) type 1-based vector has been used to deliver a reporter gene to the eyes of primates (Liu, X. et al. (1999) Exp. Eye Res.169:385-395). The construction of a HSV-1 virus vector has also been disclosed in detail in U.S. Patent Number 5,804,413 to DeLuca ("Herpes simplex virus strains for gene transfer"), which is hereby incorporated by reference. U.S. Patent Number 5,804,413 teaches the use of recombinant HSV d92 which consists of a genome containing at least one exogenous gene to be transferred to a cell under the control of the appropriate promoter for purposes including human gene therapy. Also taught by this patent are the construction and use of recombinant HSV strains deleted for ICP4, ICP27 and ICP22. For HSV vectors, see also Goins, W. F. et al. 1999 J. Virol. 73:519-532 and Xu, H. et al., (1994) Dev. Biol. 163:152-161, hereby incorporated by reference. The manipulation of cloned herpesvirus sequences, the generation of recombinant virus following the transfection of multiple plasmids containing different segments of the large herpesvirus genomes, the growth and propagation of herpesvirus, and the infection of cells with herpesvirus are techniques well known to those of ordinary skill in the art.

In another alternative, an alphavirus (positive, single-stranded RNA virus) vector is used to deliver sptm to target cells. The biology of the prototypic alphavirus, Semliki Forest Virus (SFV), has been studied extensively and gene transfer vectors have been based on the SFV genome (Garoff, H. and Li, K-J. (1998) Curr. Opin. Biotech. 9:464-469). During alphavirus RNA replication, a subgenomic RNA is generated that normally encodes the viral capsid proteins. This subgenomic RNA replicates to higher levels than the full-length genomic RNA, resulting in the overproduction of capsid proteins relative to the viral proteins with enzymatic activity (e.g., protease and polymerase). Similarly, inserting sptm into the alphavirus genome in place of the capsid-coding region results in the production of a large number of sptm RNAs and the synthesis of high levels of SPTM in vector transduced cells. While alphavirus infection is typically associated with cell lysis within a few days, the ability to establish a persistent infection in hamster normal kidney cells (BHK-21) with a variant of Sindbis virus (SIN) indicates that the lytic replication of alphaviruses can be altered to suit the needs of the gene therapy application (Dryga, S.A. et al. (1997) Virology 228:74-83). The wide host range of alphaviruses will allow the introduction of sptm into a variety of cell types. The specific transduction

(Rossi, F.M.V. and Blau, H.M. supra), or (iii) a tissue-specific promoter or the native promoter of the endogenous gene encoding SPTM from a normal individual.

Commercially available liposome transformation kits (e.g., the PERFECT LIPID TRANSFECTION KIT, available from Invitrogen) allow one with ordinary skill in the art to deliver polynucleotides to target cells in culture and require minimal effort to optimize experimental parameters. In the alternative, transformation is performed using the calcium phosphate method (Graham, F.L. and Eb, A.J. (1973) Virology 52:456-467), or by electroporation (Neumann, E. et al. (1982) EMBO J. 1:841-845). The introduction of DNA to primary cells requires modification of these standardized mammalian transfection protocols.

In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to sptm expression are treated by constructing a retrovirus vector consisting of (i) sptm under the control of an independent promoter or the retrovirus long terminal repeat (LTR) promoter, (ii) appropriate RNA packaging signals, and (iii) a Rev-responsive element (RRE) along with additional retrovirus *cis*-acting RNA sequences and coding sequences required for efficient vector propagation. Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) Proc. Natl. Acad. Sci. U.S.A. 92:6733-6737), incorporated by reference herein. The vector is propagated in an appropriate vector producing cell line (VPCL) that expresses an envelope gene with a tropism for receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al. (1987) J. Virol. 61:1647-1650; Bender, M.A. et al. (1987) J. Virol. 61:1639-1646; Adam, M.A. and Miller, A.D. (1988) J. Virol. 62:3802-3806; Dull, T. et al. (1998) J. Virol. 72:8463-8471; Zufferey, R. et al. (1998) J. Virol. 72:9873-9880). U.S. Patent Number 5,910,434 to Rigg ("Method for obtaining retrovirus packaging cell lines producing high transducing efficiency retroviral supernatant") discloses a method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference. Propagation of retrovirus vectors, transduction of a population of cells (e.g., $CD4^+$ T-cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) J. Virol. 71:7020-7029; Bauer, G. et al. (1997) Blood 89:2259-2267; Bonyhadi, M.L. (1997) J. Virol. 71:4707-4716; Ranga, U. et al. (1998) Proc. Natl. Acad. Sci. U.S.A. 95:1201-1206; Su, L. (1997) Blood 89:2283-2290).

In the alternative, an adenovirus-based gene therapy delivery system is used to deliver sptm to cells which have one or more genetic abnormalities with respect to the expression of sptm. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill in the art. Replication defective adenovirus vectors have proven to be versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas (Csete, M.E. et al. (1995) Transplantation 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent

cells are then used to produce hybridomas using standard techniques. About 20 mg of peptide is sufficient for labeling and screening several thousand clones. Hybridomas of interest are detected by screening with radioiodinated peptide to identify those fusions producing peptide-specific monoclonal antibody. In a typical protocol, wells of a multi-well plate (FAST, Becton-Dickinson, Palo Alto, CA) are coated with affinity-purified, specific rabbit-anti-mouse (or suitable anti-species IgG) antibodies at 10 mg/ml. The coated wells are blocked with 1% BSA and washed and exposed to supernatants from hybridomas. After incubation, the wells are exposed to radiolabeled peptide at 1 mg/ml.

Clones producing antibodies bind a quantity of labeled peptide that is detectable above background. Such clones are expanded and subjected to 2 cycles of cloning. Cloned hybridomas are injected into pristane-treated mice to produce ascites, and monoclonal antibody is purified from the ascitic fluid by affinity chromatography on protein A (Amersham Pharmacia Biotech). Several procedures for the production of monoclonal antibodies, including in vitro production, are described in Pound (supra). Monoclonal antibodies with antipeptide activity are tested for anti-SPTM activity using protocols well known in the art, including ELISA, RIA, and immunoblotting.

Antibody fragments containing specific binding sites for an epitope may also be generated. For example, such fragments include, but are not limited to, the F(ab')2 fragments produced by pepsin digestion of the antibody molecule, and the Fab fragments generated by reducing the disulfide bridges of the F(ab')2 fragments. Alternatively, construction of Fab expression libraries in filamentous bacteriophage allows rapid and easy identification of monoclonal fragments with desired specificity (Pound, supra, Chaps. 45-47). Antibodies generated against polypeptide encoded by sptm can be used to purify and characterize full-length SPTM protein and its activity, binding partners, etc.

Assays Using Antibodies

Anti-SPTM antibodies may be used in assays to quantify the amount of SPTM found in a particular human cell. Such assays include methods utilizing the antibody and a label to detect expression level under normal or disease conditions. The peptides and antibodies of the invention may be used with or without modification or labeled by joining them, either covalently or noncovalently, with a reporter molecule.

Protocols for detecting and measuring protein expression using either polyclonal or monoclonal antibodies are well known in the art. Examples include ELISA, RIA, and fluorescent activated cell sorting (FACS). Such immunoassays typically involve the formation of complexes between the SPTM and its specific antibody and the measurement of such complexes. These and other assays are described in Pound (supra).

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific

of a subset of cells in a population may require the sorting of cells prior to transduction. The methods of manipulating infectious cDNA clones of alphaviruses, performing alphavirus cDNA and RNA transfections, and performing alphavirus infections, are well known to those with ordinary skill in the art.

Antibodies

Anti-SPTM antibodies may be used to analyze protein expression levels. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, and Fab fragments. For descriptions of and protocols of antibody technologies, see, e.g., Pound J.D. (1998) Immunochemical Protocols, Humana Press, Totowa, NJ.

The amino acid sequence encoded by the sptm of the Sequence Listing may be analyzed by appropriate software (e.g., LASERGENE NAVIGATOR software, DNASTAR) to determine regions of high immunogenicity. The optimal sequences for immunization are selected from the C-terminus, the N-terminus, and those intervening, hydrophilic regions of the polypeptide which are likely to be exposed to the external environment when the polypeptide is in its natural conformation. Analysis used to select appropriate epitopes is also described by Ausubel (1997, supra, Chapter 11.7). Peptides used for antibody induction do not need to have biological activity; however, they must be antigenic. Peptides used to induce specific antibodies may have an amino acid sequence consisting of at five amino acids, preferably at least 10 amino acids, and most preferably 15 amino acids. A peptide which mimics an antigenic fragment of the natural polypeptide may be fused with another protein such as keyhole limpet cyanin (KLH; Sigma, St. Louis MO) for antibody production. A peptide encompassing an antigenic region may be expressed from an sptm, synthesized as described above, or purified from human cells.

Procedures well known in the art may be used for the production of antibodies. Various hosts including mice, goats, and rabbits, may be immunized by injection with a peptide. Depending on the host species, various adjuvants may be used to increase immunological response.

In one procedure, peptides about 15 residues in length may be synthesized using an ABI 431A peptide synthesizer (PE Biosystems) using fmoc-chemistry and coupled to KLH (Sigma) by reaction with M-maleimidobenzoyl-N-hydroxysuccinimide ester (Ausubel, 1995, supra). Rabbits are immunized with the peptide-KLH complex in complete Freund's adjuvant. The resulting antisera are tested for antipeptide activity by binding the peptide to plastic, blocking with 1% bovine serum albumin (BSA), reacting with rabbit antisera, washing, and reacting with radioiodinated goat anti-rabbit IgG. Antisera with antipeptide activity are tested for anti-SPTM activity using protocols well known in the art, including ELISA, radioimmunoassay (RIA), and immunoblotting.

In another procedure, isolated and purified peptide may be used to immunize mice (about 100 µg of peptide) or rabbits (about 1 mg of peptide). Subsequently, the peptide is radioiodinated and used to screen the immunized animals' B-lymphocytes for production of antipeptide antibodies. Positive

Plasmids were recovered from host cells by in vivo excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: the Magic or WIZARD Minipreps DNA purification system (Promega); the AGTC Miniprep purification kit (Edge BioSystems, Gaithersburg MD); and the QIAWELL 8, QIAWELL 8 Plus, and QIAWELL 8 Ultra plasmid purification systems or the R.E.A.L. PREP 96 plasmid purification kit (QIAGEN). Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format. (Rao, V.B. (1994) Anal. Biochem. 216:1-14.) Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Inc. (Molecular Probes), Eugene OR) and a FLUOROSKAN II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

III. Sequencing and Analysis

cDNA sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 thermal cycler (PE Biosystems) or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific Corp., Sunnyvale CA) or the MICROLAB 2200 liquid transfer system (Hamilton). cDNA sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (PE Biosystems). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the ABI PRISM 373 or 377 sequencing system (PE Biosystems) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art. Reading frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, supra, Chapter 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example VIII.

IV. Assembly and Analysis of Sequences

Component sequences from chromatograms were subject to PHRED analysis and assigned a quality score. The sequences having at least a required quality score were subject to various pre-processing editing pathways to eliminate, e.g., low quality 3' ends, vector and linker sequences, polyA tails, Alu repeats, mitochondrial and ribosomal sequences, bacterial contamination sequences, and sequences smaller than 50 base pairs. In particular, low-information sequences and repetitive elements (e.g., dinucleotide repeats, Alu repeats, etc.) were replaced by "n's", or masked, to prevent spurious matches.

embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications, and publications mentioned above and below, in particular U.S. Ser. No. 60/156,624, U.S. Ser. No. 60/156,625, U.S. Ser. No. 60/168,614, U.S. Ser. No. 60/168,611, and U.S. Ser. No. 60/168,613 are hereby expressly incorporated by reference.

EXAMPLES

I. Construction of cDNA Libraries

RNA was purchased from CLONTECH Laboratories, Inc. (Palo Alto CA) or isolated from various tissues. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In most cases, RNA was treated with DNase. For most libraries, poly(A+) RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega Corporation (Promega), Madison WI), OLIGOTEX latex particles (QIAGEN, Inc. (QIAGEN), Valencia CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Inc., Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene Cloning Systems, Inc. (Stratagene), La Jolla CA) or SUPERSCRIPT plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, supra, Chapters 5.1 through 6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUESCRIPT plasmid (Stratagene), pSPORT1 plasmid (Life Technologies), or pINCY (Incyte). Recombinant plasmids were transformed into competent E. coli cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5α, DH10B, or ElectroMAX DH10B from Life Technologies.

II. Isolati n of cDNA Clones

Following assembly, template sequences were subjected to motif, BLAST, and functional analyses, and categorized in protein hierarchies using methods described in, e.g., "Database System Employing Protein Function Hierarchies for Viewing Biomolecular Sequence Data," U.S.S.N. 08/812,290, filed March 6, 1997; "Relational Database for Storing Biomolecule Information," U.S.S.N. 08/947,845, filed October 9, 1997; "Project-Based Full-Length Biomolecular Sequence Database," U.S.S.N. 08/811,758, filed March 6, 1997; and "Relational Database and System for Storing Information Relating to Biomolecular Sequences," U.S.S.N. 09/034,807, filed March 4, 1998, all of which are incorporated by reference herein.

The template sequences were further analyzed by translating each template in all three forward reading frames and searching each translation against the Pfam database of hidden Markov model-based protein families and domains using the HMMER software package (available to the public from Washington University School of Medicine, St. Louis MO). (See also World Wide Web site http://pfam.wustl.edu/ for detailed descriptions of Pfam protein domains and families.)

Additionally, the template sequences were translated in all three forward reading frames, and each translation was searched against hidden Markov models for signal peptide and transmembrane domains using the HMMER software package. Construction of hidden Markov models and their usage in sequence analysis has been described. (See, for example, Eddy, S.R. (1996) Curr. Opin. Str. Biol. 6:361-365.) Regions of templates which, when translated, contain similarity to signal peptide or transmembrane domain consensus sequences are reported in Table 1. Only those signal peptide or transmembrane hits with a cutoff score of 11 bits or greater are reported. A cutoff score of 11 bits or greater corresponds to at least about 91-94% true-positives in signal peptide prediction, and at least about 75% true-positives in transmembrane domain prediction.

Template sequences are further analyzed using the bioinformatics tools listed in Table 4, or using sequence analysis software known in the art such as MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Template sequences may be further queried against public databases such as the GenBank rodent, mammalian, vertebrate, prokaryote, and eukaryote databases.

V. Analysis of Polynucleotide Expression

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, supra, ch. 7; Ausubel, 1995, supra, ch. 4 and 16.)

Analogous computer techniques applying BLAST were used to search for identical or related molecules in cDNA databases such as GenBank or LIFESEQ (Incyte Genomics). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer

Processed sequences were then subject to assembly procedures in which the sequences were assigned to gene bins (bins). Each sequence could only belong to one bin. Sequences in each gene bin were assembled to produce consensus sequences (templates). Subsequent new sequences were added to existing bins using BLASTn (v.1.4 WashU) and CROSSMATCH. Candidate pairs were identified as all BLAST hits having a quality score greater than or equal to 150. Alignments of at least 82% local identity were accepted into the bin. The component sequences from each bin were assembled using a version of PHRAP. Bins with several overlapping component sequences were assembled using DEEP PHRAP. The orientation (sense or antisense) of each assembled template was determined based on the number and orientation of its component sequences. Template sequences as disclosed in the sequence listing correspond to sense strand sequences (the "forward" reading frames), to the best determination. The complementary (antisense) strands are inherently disclosed herein. The component sequences which were used to assemble each template consensus sequence are listed in Table 2, along with their positions along the template nucleotide sequences.

Bins were compared against each other and those having local similarity of at least 82% were combined and reassembled. Reassembled bins having templates of insufficient overlap (less than 95% local identity) were re-split. Assembled templates were also subject to analysis by STITCHER/EXON MAPPER algorithms which analyze the probabilities of the presence of splice variants, alternatively spliced exons, splice junctions, differential expression of alternative spliced genes across tissue types or disease states, etc. These resulting bins were subject to several rounds of the above assembly procedures.

Once gene bins were generated based upon sequence alignments, bins were clone joined based upon clone information. If the 5' sequence of one clone was present in one bin and the 3' sequence from the same clone was present in a different bin, it was likely that the two bins actually belonged together in a single bin. The resulting combined bins underwent assembly procedures to regenerate the consensus sequences.

The final assembled templates were subsequently annotated using the following procedure. Template sequences were analyzed using BLASTn (v2.0, NCBI) versus gbpri (GenBank version 118). "Hits" were defined as an exact match having from 95% local identity over 200 base pairs through 100% local identity over 100 base pairs, or a homolog match having an E-value, i.e. a probability score, of $\leq 1 \times 10^{-8}$. The hits were subject to frameshift FASTx versus GENPEPT (GenBank version 118). (See Table 4). In this analysis, a homolog match was defined as having an E-value of $\leq 1 \times 10^{-8}$. The assembly method used above was described in "System and Methods for Analyzing Biomolecular Sequences," U.S.S.N. 09/276,534, filed March 25, 1999, and the LIFESEQ Gold user manual (Incyte) both incorporated by reference herein.

sequences and cDNA library/tissue information are found in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA).

VI. Tissue Distribution Profiling

A tissue distribution profile is determined for each template by compiling the cDNA library tissue classifications of its component cDNA sequences. Each component sequence, is derived from a cDNA library constructed from a human tissue. Each human tissue is classified into one of the following categories: cardiovascular system; connective tissue; digestive system; embryonic structures; endocrine system; exocrine glands; genitalia, female; genitalia, male; germ cells; hemic and immune system; liver; musculoskeletal system; nervous system; pancreas; respiratory system; sense organs; skin; stomatognathic system; unclassified/mixed; or urinary tract. Template sequences, component sequences, and cDNA library/tissue information are found in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA).

Table 3 shows the tissue distribution profile for the templates of the invention. For each template, the three most frequently observed tissue categories are shown in column 3, along with the percentage of component sequences belonging to each category. Only tissue categories with percentage values of ≥10% are shown. A tissue distribution of "widely distributed" in column 3 indicates percentage values of <10% in all tissue categories.

VII. Transcript Image Analysis

Transcript images are generated as described in Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, incorporated herein by reference.

VIII. Extension of Polynucleotide Sequences and Isolation of a Full-length cDNA

Oligonucleotide primers designed using an sptm of the Sequence Listing are used to extend the nucleic acid sequence. One primer is synthesized to initiate 5' extension of the template, and the other primer, to initiate 3' extension of the template. The initial primers may be designed using OLIGO 4.06 software (National Biosciences, Inc. (National Biosciences), Plymouth MN), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations are avoided. Selected human cDNA libraries are used to extend the sequence. If more than one extension is necessary or desired, additional or nested sets of primers are designed.

High fidelity amplification is obtained by PCR using methods well known in the art. PCR is performed in 96-well plates using the PTC-200 thermal cycler (MJ Research). The reaction mix contains DNA template, 200 nmol of each primer, reaction buffer containing Mg^{2+}, $(NH_4)_2SO_4$, and β-mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme (Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair

search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

$$\frac{\text{BLAST Score} \times \text{Percent Identity}}{5 \times \text{minimum } \{\text{length(Seq. 1)}, \text{length(Seq. 2)}\}}$$

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. The product score is a normalized value between 0 and 100, and is calculated as follows: the BLAST score is multiplied by the percent nucleotide identity and the product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is calculated by assigning a score of +5 for every base that matches in a high-scoring segment pair (HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate the product score. The product score represents a balance between fractional overlap and quality in a BLAST alignment. For example, a product score of 100 is produced only for 100% identity over the entire length of the shorter of the two sequences being compared. A product score of 70 is produced either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or 79% identity and 100% overlap.

Alternatively, polynucleotide sequences encoding SPTM are analyzed with respect to the tissue sources from which they were derived. Polynucleotide sequences encoding SPTM were assembled, at least in part, with overlapping Incyte cDNA sequences. Each cDNA sequence is derived from a cDNA library constructed from a human tissue. Each human tissue is classified into one of the following organ/tissue categories: cardiovascular system; connective tissue; digestive system; embryonic structures; endocrine system; exocrine glands; genitalia, female; genitalia, male; germ cells; hemic and immune system; liver; musculoskeletal system; nervous system; pancreas; respiratory system; sense organs; skin; stomatognathic system; unclassified/mixed; or urinary tract. The number of libraries in each category for each polynucleotide sequence encoding SPTM is counted and divided by the total number of libraries across all categories for each polynucleotide sequence encoding SPTM. Similarly, each human tissue is classified into one of the following disease/condition categories: cancer, cell line, developmental, inflammation, neurological, trauma, cardiovascular, pooled, and other, and the number of libraries in each category for each polynucleotide sequence encoding SPTM is counted and divided by the total number of libraries across all categories for each polynucleotide sequence encoding SPTM. The resulting percentages reflect the tissue- and disease-specific expression of cDNA encoding SPTM. Percentage values of tissue-specific and disease-specific expression are reported in Table 3. cDNA

Hybridization probes derived from the sptm of the Sequence Listing are employed for screening cDNAs, mRNAs, or genomic DNA. The labeling of probe nucleotides between 100 and 1000 nucleotides in length is specifically described, but essentially the same procedure may be used with larger cDNA fragments. Probe sequences are labeled at room temperature for 30 minutes using a T4 polynucleotide kinase, γ^{32}P-ATP, and 0.5X One-Phor-All Plus (Amersham Pharmacia Biotech) buffer and purified using a ProbeQuant G-50 Microcolumn (Amersham Pharmacia Biotech). The probe mixture is diluted to 10^7 dpm/µg/ml hybridization buffer and used in a typical membrane-based hybridization analysis.

The DNA is digested with a restriction endonuclease such as Eco RV and is electrophoresed through a 0.7% agarose gel. The DNA fragments are transferred from the agarose to nylon membrane (NYTRAN Plus, Schleicher & Schuell, Inc., Keene NH) using procedures specified by the manufacturer of the membrane. Prehybridization is carried out for three or more hours at 68°C, and hybridization is carried out overnight at 68°C. To remove non-specific signals, blots are sequentially washed at room temperature under increasingly stringent conditions, up to 0.1x saline sodium citrate (SSC) and 0.5% sodium dodecyl sulfate. After the blots are placed in a PHOSPHORIMAGER cassette (Molecular Dynamics) or are exposed to autoradiography film, hybridization patterns of standard and experimental lanes are compared. Essentially the same procedure is employed when screening RNA.

X. Chromosome Mapping of sptm

The cDNA sequences which were used to assemble SEQ ID NO:1-63 are compared with sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other implementations of the Smith-Waterman algorithm. Sequences from these databases that match SEQ ID NO:1-63 are assembled into clusters of contiguous and overlapping sequences using assembly algorithms such as PHRAP (Table 4). Radiation hybrid and genetic mapping data available from public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for Genome Research (WIGR), and Généthon are used to determine if any of the clustered sequences have been previously mapped. Inclusion of a mapped sequence in a cluster will result in the assignment of all sequences of that cluster, including its particular SEQ ID NO:, to that map location. The genetic map locations of SEQ ID NO:1-63 are described as ranges, or intervals, of human chromosomes. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Généthon which provide boundaries for radiation hybrid markers whose sequences were included in each of the clusters.

XI. Micr array Analysis

PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ are as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well is determined by dispensing 100 µl PICOGREEN quantitation reagent (0.25% (v/v); Molecular Probes) dissolved in 1X Tris-EDTA (TE) and 0.5 µl of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Incorporated (Corning), Corning NY), allowing the DNA to bind to the reagent. The plate is scanned in a FLUOROSKAN II (Labsystems Oy) to measure the fluorescence of the sample and to quantify theconcentration of DNA. A 5 µl to 10 µl aliquot of the reaction mixture is analyzed by electrophoresis on a 1 % agarose mini-gel to determine which reactions are successful in extending the sequence.

The extended nucleotides are desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For shotgun sequencing, the digested nucleotides are separated on low concentration (0.6 to 0.8%) agarose gels, fragments are excised, and agar digested with AGAR ACE (Promega). Extended clones are religated using T4 ligase (New England Biolabs, Inc., Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent E. coli cells. Transformed cells are selected on antibiotic-containing media, individual colonies are picked and cultured overnight at 37°C in 384-well plates in LB/2x carbenicillin liquid media.

The cells are lysed, and DNA is amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA is quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries are reamplified using the same conditions as described above. Samples are diluted with 20% dimethysulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (PE Biosystems).

In like manner, the sptm is used to obtain regulatory sequences (promoters, introns, and enhancers) using the procedure above, oligonucleotides designed for such extension, and an appropriate genomic library.

IX. Labeling f Pr bes and S uthern Hybridization Analyses

Microarrays are UV-crosslinked using a STRATALINKER UV-crosslinker (Stratagene). Microarrays are washed at room temperature once in 0.2% SDS and three times in distilled water. Non-specific binding sites are blocked by incubation of microarrays in 0.2% casein in phosphate buffered saline (PBS) (Tropix, Inc., Bedford, MA) for 30 minutes at 60° C followed by washes in 0.2% SDS and distilled water as before.

Hybridization

Hybridization reactions contain 9 µl of probe mixture consisting of 0.2 µg each of Cy3 and Cy5 labeled cDNA synthesis products in 5X SSC, 0.2% SDS hybridization buffer. The probe mixture is heated to 65° C for 5 minutes and is aliquoted onto the microarray surface and covered with an 1.8 cm^2 coverslip. The arrays are transferred to a waterproof chamber having a cavity just slightly larger than a microscope slide. The chamber is kept at 100% humidity internally by the addition of 140 µl of 5x SSC in a corner of the chamber. The chamber containing the arrays is incubated for about 6.5 hours at 60° C. The arrays are washed for 10 min at 45° C in a first wash buffer (1X SSC, 0.1% SDS), three times for 10 minutes each at 45° C in a second wash buffer (0.1X SSC), and dried.

Detection

Reporter-labeled hybridization complexes are detected with a microscope equipped with an Innova 70 mixed gas 10 W laser (Coherent, Inc., Santa Clara CA) capable of generating spectral lines at 488 nm for excitation of Cy3 and at 632 nm for excitation of Cy5. The excitation laser light is focused on the array using a 20X microscope objective (Nikon, Inc., Melville NY). The slide containing the array is placed on a computer-controlled X-Y stage on the microscope and raster-scanned past the objective. The 1.8 cm x 1.8 cm array used in the present example is scanned with a resolution of 20 micrometers.

In two separate scans, a mixed gas multiline laser excites the two fluorophores sequentially. Emitted light is split, based on wavelength, into two photomultiplier tube detectors (PMT R1477, Hamamatsu Photonics Systems, Bridgewater NJ) corresponding to the two fluorophores. Appropriate filters positioned between the array and the photomultiplier tubes are used to filter the signals. The emission maxima of the fluorophores used are 565 nm for Cy3 and 650 nm for Cy5. Each array is typically scanned twice, one scan per fluorophore using the appropriate filters at the laser source, although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

The sensitivity of the scans is typically calibrated using the signal intensity generated by a cDNA control species added to the probe mix at a known concentration. A specific location on the array contains a complementary DNA sequence, allowing the intensity of the signal at that location to be correlated with a weight ratio of hybridizing species of 1:100,000. When two probes from different sources (e.g., representing test and control cells), each labeled with a different fluorophore, are hybridized to a single array for the purpose of identifying genes that are differentially expressed, the

Probe Preparation from Tissue or Cell Samples

Total RNA is isolated from tissue samples using the guanidinium thiocyanate method and polyA$^+$ RNA is purified using the oligo (dT) cellulose method. Each polyA$^+$ RNA sample is reverse transcribed using MMLV reverse-transcriptase, 0.05 pg/µl oligo-dT primer (21mer), 1X first strand buffer, 0.03 units/µl RNase inhibitor, 500 µM dATP, 500 µM dGTP, 500 µM dTTP, 40 µM dCTP, 40 µM dCTP-Cy3 (BDS) or dCTP-Cy5 (Amersham Pharmacia Biotech). The reverse transcription reaction is performed in a 25 ml volume containing 200 ng polyA$^+$ RNA with GEMBRIGHT kits (Incyte). Specific control polyA$^+$ RNAs are synthesized by in vitro transcription from non-coding yeast genomic DNA (W. Lei, unpublished). As quantitative controls, the control mRNAs at 0.002 ng, 0.02 ng, 0.2 ng, and 2 ng are diluted into reverse transcription reaction at ratios of 1:100,000, 1:10,000, 1:1000, 1:100 (w/w) to sample mRNA respectively. The control mRNAs are diluted into reverse transcription reaction at ratios of 1:3, 3:1, 1:10, 10:1, 1:25, 25:1 (w/w) to sample mRNA differential expression patterns. After incubation at 37°C for 2 hr, each reaction sample (one with Cy3 and another with Cy5 labeling) is treated with 2.5 ml of 0.5M sodium hydroxide and incubated for 20 minutes at 85°C to the stop the reaction and degrade the RNA. Probes are purified using two successive CHROMA SPIN 30 gel filtration spin columns (CLONTECH Laboratories, Inc. (CLONTECH), Palo Alto CA) and after combining, both reaction samples are ethanol precipitated using 1 ml of glycogen (1 mg/ml), 60 ml sodium acetate, and 300 ml of 100% ethanol. The probe is then dried to completion using a SpeedVAC (Savant Instruments Inc., Holbrook NY) and resuspended in 14 µl 5X SSC/0.2% SDS.

Microarray Preparation

Sequences of the present invention are used to generate array elements. Each array element is amplified from bacterial cells containing vectors with cloned cDNA inserts. PCR amplification uses primers complementary to the vector sequences flanking the cDNA insert. Array elements are amplified in thirty cycles of PCR from an initial quantity of 1-2 ng to a final quantity greater than 5 µg. Amplified array elements are then purified using SEPHACRYL-400 (Amersham Pharmacia Biotech).

Purified array elements are immobilized on polymer-coated glass slides. Glass microscope slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR Scientific Products Corporation (VWR), West Chester, PA), washed extensively in distilled water, and coated with 0.05% aminopropyl silane (Sigma) in 95% ethanol. Coated slides are cured in a 110°C oven.

Array elements are applied to the coated glass substrate using a procedure described in US Patent No. 5,807,522, incorporated herein by reference. 1 µl of the array element DNA, at an average concentration of 100 ng/µl, is loaded into the open capillary printing element by a high-speed robotic apparatus. The apparatus then deposits about 5 nl of array element sample per slide.

transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See e.g., Engelhard, supra; and Sandig, supra.)

In most expression systems, SPTM is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from SPTM at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak Company, Rochester NY). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, Chapters 10 and 16). Purified SPTM obtained by these methods can be used directly in the following activity assay.

XIV. Demonstration of SPTM Activity

An assay for SPTM activity measures the expression of SPTM on the cell surface. cDNA encoding SPTM is subcloned into an appropriate mammalian expression vector suitable for high levels of cDNA expression. The resulting construct is transfected into a nonhuman cell line such as NIH3T3. Cell surface proteins are labeled with biotin using methods known in the art. Immunoprecipitations are performed using SPTM-specific antibodies, and immunoprecipitated samples are analyzed using SDS-PAGE and immunoblotting techniques. The ratio of labeled immunoprecipitant to unlabeled immunoprecipitant is proportional to the amount of SPTM expressed on the cell surface.

Alternatively, an assay for SPTM activity measures the amount of SPTM in secretory, membrane-bound organelles. Transfected cells as described above are harvested and lysed. The lysate is fractionated using methods known to those of skill in the art, for example, sucrose gradient ultracentrifugation. Such methods allow the isolation of subcellular components such as the Golgi apparatus, ER, small membrane-bound vesicles, and other secretory organelles. Immunoprecipitations from fractionated and total cell lysates are performed using SPTM-specific antibodies, and immunoprecipitated samples are analyzed using SDS-PAGE and immunoblotting techniques. The concentration of SPTM in secretory organelles relative to SPTM in total cell lysate is proportional to the amount of SPTM in transit through the secretory pathway.

XV. Functi nal Assays

calibration is done by labeling samples of the calibrating cDNA with the two fluorophores and adding identical amounts of each to the hybridization mixture.

The output of the photomultiplier tube is digitized using a 12-bit RTI-835H analog-to-digital (A/D) conversion board (Analog Devices, Inc., Norwood, MA) installed in an IBM-compatible PC computer. The digitized data are displayed as an image where the signal intensity is mapped using a linear 20-color transformation to a pseudocolor scale ranging from blue (low signal) to red (high signal). The data is also analyzed quantitatively. Where two different fluorophores are excited and measured simultaneously, the data are first corrected for optical crosstalk (due to overlapping emission spectra) between the fluorophores using each fluorophore's emission spectrum.

A grid is superimposed over the fluorescence signal image such that the signal from each spot is centered in each element of the grid. The fluorescence signal within each element is then integrated to obtain a numerical value corresponding to the average intensity of the signal. The software used for signal analysis is the GEMTOOLS gene expression analysis program (Incyte).

XII. Complementary Nucleic Acids

Sequences complementary to the sptm are used to detect, decrease, or inhibit expression of the naturally occurring nucleotide. The use of oligonucleotides comprising from about 15 to 30 base pairs is typical in the art. However, smaller or larger sequence fragments can also be used. Appropriate oligonucleotides are designed from the sptm using OLIGO 4.06 software (National Biosciences) or other appropriate programs and are synthesized using methods standard in the art or ordered from a commercial supplier. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent transcription factor binding to the promoter sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding and processing of the transcript.

XIII. Expression of SPTM

Expression and purification of SPTM is accomplished using bacterial or virus-based expression systems. For expression of SPTM in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac* (*tac*) hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express SPTM upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of SPTM in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding SPTM by either homologous recombination or bacterial-mediated

Alternatively, the SPTM amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding peptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, supra, Chapter 11.)

Typically, peptides 15 residues in length are synthesized using an ABI 431A peptide synthesizer (PE Biosystems) using fmoc-chemistry and coupled to KLH (Sigma) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, supra.) Rabbits are immunized with the peptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for antipeptide activity by, for example, binding the peptide to plastic, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG. Antisera with antipeptide activity are tested for anti-SPTM activity using protocols well known in the art, including ELISA, RIA, and immunoblotting.

XVII. Purification of Naturally Occurring SPTM Using Specific Antibodies

Naturally occurring or recombinant SPTM is substantially purified by immunoaffinity chromatography using antibodies specific for SPTM. An immunoaffinity column is constructed by covalently coupling anti-SPTM antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing SPTM are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of SPTM (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/SPTM binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and SPTM is collected.

XVIII. Identification of Molecules Which Interact with SPTM

SPTM, or biologically active fragments thereof, are labeled with ^{125}I Bolton-Hunter reagent. (See, e.g., Bolton, A.E. and W.M. Hunter (1973) Biochem. J. 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled SPTM, washed, and any wells with labeled SPTM complex are assayed. Data obtained using different concentrations of SPTM are used to calculate values for the number, affinity, and association of SPTM with the candidate molecules.

Alternatively, molecules interacting with SPTM are analyzed using the yeast two-hybrid system as described in Fields, S. and O. Song (1989) Nature 340:245-246, or using commercially available kits based on the two-hybrid system, such as the MATCHMAKER system (CLONTECH).

SPTM function is assessed by expressing sptm at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include pCMV SPORT (Life Technologies) and pCR3.1 (Invitrogen Corporation, Carlsbad CA), both of which contain the cytomegalovirus promoter. 5-10 µg of recombinant vector are transiently transfected into a human cell line, preferably of endothelial or hematopoietic origin, using either liposome formulations or electroporation. 1-2 µg of an additional plasmid containing sequences encoding a marker protein are co-transfected.

Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; CLONTECH), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties.

FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M. G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of SPTM on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding SPTM and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Inc., Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding SPTM and other genes of interest can be analyzed by northern analysis or microarray techniques.

XVI. Production of Antibodies

SPTM substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) Methods Enzymol. 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

Table 1

SEQ ID NO	Template ID	Start	Stop	Frame	Domain Type
1	198450.6.oct	272	343	forward 2	TM
1	198450.6.oct	269	334	forward 2	SP
1	198450.6.oct	263	346	forward 2	TM
2	475178.1.oct	1233	1292	forward 3	SP
2	475178.1.oct	95	172	forward 2	SP
2	475178.1.oct	1221	1274	forward 3	SP
2	475178.1.oct	95	157	forward 2	SP
3	231793.2.oct	739	801	forward 1	SP
3	231793.2.oct	739	810	forward 1	SP
3	231793.2.oct	865	930	forward 1	SP
3	231793.2.oct	739	810	forward 1	SP
3	231793.2.oct	730	810	forward 1	SP
4	000010.4.oct	1637	1684	forward 2	SP
4	000010.4.oct	1637	1696	forward 2	SP
5	412959.6.oct	329	409	forward 2	TM
5	412959.6.oct	586	642	forward 1	SP
5	412959.6.oct	350	406	forward 2	TM
6	331521.5.oct	807	860	forward 3	TM
6	331521.5.oct	840	902	forward 3	SP
7	902114.1.oct	288	341	forward 3	SP
7	902114.1.oct	288	338	forward 3	SP
7	902114.1.oct	288	353	forward 3	SP
7	902114.1.oct	288	347	forward 3	SP
8	481382.1.oct	730	798	forward 1	SP
8	481382.1.oct	730	789	forward 1	SP
9	903849.1.oct	1361	1414	forward 2	TM
9	903849.1.oct	1338	1403	forward 3	SP
10	433776.4.oct	737	802	forward 2	SP
10	433776.4.oct	797	892	forward 2	SP
11	407607.4.oct	1634	1687	forward 2	TM
11	407607.4.oct	1429	1500	forward 1	SP
12	234828.6.oct	1091	1180	forward 2	SP
12	234828.6.oct	1115	1189	forward 2	SP
13	336430.2.dec	1290	1355	forward 3	SP
13	336430.2.dec	857	931	forward 2	SP
13	336430.2.dec	749	850	forward 2	SP
14	242269.2.dec	769	837	forward 1	TM
15	432120.2.dec	503	559	forward 2	TM
16	198060.6.dec	40	126	forward 1	SP
17	460295.5.dec	369	449	forward 3	TM
18	235983.6.dec	3319	3375	forward 1	TM
18	235983.6.dec	900	953	forward 3	SP
18	235983.6.dec	3488	3565	forward 2	SP
18	235983.6.dec	3328	3390	forward 1	TM
18	235983.6.dec	4361	4414	forward 2	SP
18	235983.6.dec	2168	2236	forward 2	TM
18	235983.6.dec	4340	4420	forward 2	SP
18	235983.6.dec	4361	4435	forward 2	SP
18	235983.6.dec	4379	4426	forward 2	SP
18	235983.6.dec	4361	4426	forward 2	SP
18	235983.6.dec	4361	4420	forward 2	SP
19	238703.2.dec	1057	1140	forward 1	SP
20	038751.5.dec	744	809	forward 3	TM
20	038751.5.dec	167	238	forward 2	TM
20	038751.5.dec	729	803	forward 3	SP
20	038751.5.dec	464	526	forward 2	TM
21	236099.4.dec	1254	1352	forward 3	SP
22	350875.2.dec	479	535	forward 2	TM
23	466521.5.dec	598	666	forward 1	SP
24	466521.6.dec	719	787	forward 2	SP
25	474522.8.d c	483	566	forward 3	SP
25	474522.8.dec	483	557	forward 3	SP
25	474522.8.dec	507	566	forward 3	SP
25	474522.8.dec	507	572	forward 3	SP
26	231583.3.dec	1186	1230	forward 1	TM
26	231583.3.dec	1159	1239	forward 1	TM
26	231583.3.dec	1165	1233	forward 1	SP
26	231583.3.dec	1188	1238	forward 3	TM
26	231583.3.dec	1195	1257	forward 1	TM
26	231583.3.dec	1162	1233	forward 1	TM
26	231583.3.dec	1165	1227	forward 1	SP
26	231583.3.dec	571	618	forward 1	SP
26	231583.3.dec	1195	1251	forward 1	TM
26	231583.3.dec	1184	1243	forward 2	TM
26	231583.3.dec	1170	1232	forward 3	TM
26	231583.3.dec	1182	1238	forward 3	TM
27	215051.5.dec	975	1031	forward 3	TM
27	215051.5.dec	1428	1487	forward 3	TM
27	215051.5.dec	1424	1492	forward 2	SP
27	215051.5.dec	960	1034	forward 3	SP
27	215051.5.dec	1394	1456	forward 2	TM
27	215051.5.dec	1424	1480	forward 2	SP
27	215051.5.dec	861	920	forward 3	TM
27	215051.5.dec	51	140	forward 3	SP
27	215051.5.dec	506	577	forward 2	SP
27	215051.5.dec	1421	1501	forward 2	TM
27	215051.5.dec	1424	1480	forward 2	TM
27	215051.5.dec	1412	1462	forward 2	TM
27	215051.5.dec	1424	1471	forward 2	SP
27	215051.5.dec	1424	1480	forward 2	SP
28	277726.5.dec	655	711	forward 1	TM
28	277726.5.dec	853	918	forward 1	TM
28	277726.5.dec	826	900	forward 1	TM
28	277726.5.dec	370	426	forward 1	TM
28	277726.5.dec	652	729	forward 1	TM
28	277726.5.dec	832	894	forward 1	TM
28	277726.5.dec	1377	1430	forward 3	TM
28	277726.5.dec	832	903	forward 1	TM
28	277726.5.dec	844	894	forward 1	TM
29	978637.1.dec	19	123	forward 1	SP
30	240518.12.dec	61	114	forward 1	TM
30	240518.12.dec	64	126	forward 1	TM
30	240518.12.dec	868	978	forward 1	SP
30	240518.12.dec	931	978	forward 1	SP
31	413231.8.dec	1182	1244	forward 3	SP
31	413231.8.dec	2531	2593	forward 2	TM
31	413231.8.dec	1188	1256	forward 3	SP
31	413231.8.dec	1741	1803	forward 1	TM
31	413231.8.dec	1182	1235	forward 3	SP
31	413231.8.dec	1188	1262	forward 3	SP
31	413231.8.dec	1182	1262	forward 3	SP
32	334406.5.dec	886	969	forward 1	SP
33	411429.8.dec	468	530	forward 3	TM
34	320674.7.dec	1649	1717	forward 2	TM
35	197267.1.dec	5	76	forward 2	SP
35	197267.1.dec	14	58	forward 2	SP
35	197267.1.dec	5	67	forward 2	SP
35	197267.1.dec	2	67	forward 2	SP
35	197267.1.dec	11	67	forward 2	SP
35	197267.1.dec	723	803	forward 3	SP
36	332335.1.dec	785	883	forward 2	SP
37	238992.13.dec	905	994	forward 2	SP
38	199736.1.dec	157	219	forward 1	TM
38	199736.1.dec	145	204	forward 1	TM
38	199736.1.d c	166	228	forward 1	TM
39	228864.5.dec	562	642	forward 1	SP
39	228864.5.dec	26	139	forward 2	SP
40	986539.1.dec	3	95	forward 3	SP
41	481454.4.dec	561	647	forward 3	SP
41	481454.4.d c	1239	1298	forward 3	SP

SPTM may also be used in the PATHCALLING process (CuraGen Corp., New Haven CT) which employs the yeast two-hybrid system in a high-throughput manner to determine all interactions between the proteins encoded by two large libraries of genes (Nandabalan, K. et al. (2000) U.S. Patent No. 6,057,101).

All publications and patents mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described method and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the above-described modes for carrying out the invention which are obvious to those skilled in the field of molecular biology or related fields are intended to be within the scope of the following claims.

Table 2

SEQ ID NO	TemplateID	Component ID	Start	Stop	SEQ ID NO	Template ID	Component ID	Start	Stop
1	198450.6.oct	g812858	1618	1761	1	198450.6.oct	g4293934	1338	1745
1	198450.6.oct	3133936T6	1642	1704	1	198450.6.oct	3433379H1	1343	1423
1	198450.6.oct	3765347H1	1	286	1	198450.6.oct	2730946H1	1352	1602
1	198450.6.oct	2881536H1	23	287	1	198450.6.oct	g2111659	1365	1747
1	198450.6.oct	2881536F6	23	509	1	198450.6.oct	4501340H1	1369	1614
1	198450.6.oct	3692305H1	226	529	1	198450.6.oct	g3755006	1372	1738
1	198450.6.oct	4212539H1	301	546	1	198450.6.oct	2364954H1	1388	1447
1	198450.6.oct	3451630H1	343	596	1	198450.6.oct	2364915H1	1388	1447
1	198450.6.oct	2614961F6	401	999	1	198450.6.oct	2364954F6	1388	1447
1	198450.6.oct	2614961H1	401	667	1	198450.6.oct	g1238074	1436	1739
1	198450.6.oct	g2111714	487	878	1	198450.6.oct	g2555317	1462	1743
1	198450.6.oct	g1984142	491	674	1	198450.6.oct	g1489886	1468	1745
1	198450.6.oct	g1984144	491	746	1	198450.6.oct	4640302H1	1469	1723
1	198450.6.oct	3109843H1	496	663	1	198450.6.oct	3665959H1	1471	1702
1	198450.6.oct	3109585H1	496	595	1	198450.6.oct	4872588H1	1482	1738
1	198450.6.oct	1897893H1	551	795	1	198450.6.oct	g2435210	1490	1739
1	198450.6.oct	1897530H1	551	776	1	198450.6.oct	3133936F6	1516	1734
1	198450.6.oct	5136026H1	599	872	1	198450.6.oct	3133936H1	1517	1755
1	198450.6.oct	4505381H1	627	891	1	198450.6.oct	1293778H1	1523	1739
1	198450.6.oct	5894055H1	632	895	1	198450.6.oct	g1497107	1527	1739
1	198450.6.oct	5901947H1	632	939	1	198450.6.oct	3691633H1	1538	1730
1	198450.6.oct	5698273H1	638	908	1	198450.6.oct	g2255347	1554	1809
1	198450.6.oct	3139196H1	638	911	1	198450.6.oct	g3899575	1589	1742
1	198450.6.oct	g1278047	644	1069	1	198450.6.oct	g3735471	1615	1744
1	198450.6.oct	3945278H1	700	978	2	475178.1.oct	g3109369	893	1334
1	198450.6.oct	3941342H1	700	984	2	475178.1.oct	g2106854	903	1285
1	198450.6.oct	g2015083	709	1013	2	475178.1.oct	g1886488	906	1336
1	198450.6.oct	5467754H1	745	1017	2	475178.1.oct	g4243834	921	1335
1	198450.6.oct	g1423015	756	1149	2	475178.1.oct	g3229982	932	1335
1	198450.6.oct	g1497157	778	1271	2	475178.1.oct	g2876106	933	1289
1	198450.6.oct	3706512H1	781	1071	2	475178.1.oct	g2675531	965	1330
1	198450.6.oct	4768061H1	786	1024	2	475178.1.oct	g1479394	1023	1335
1	198450.6.oct	3683925H1	795	1075	2	475178.1.oct	g2106969	1028	1335
1	198450.6.oct	5188646H1	822	1148	2	475178.1.oct	g2910156	1042	1311
1	198450.6.oct	1456401H1	868	1143	2	475178.1.oct	6430617H1	1054	1226
1	198450.6.oct	3822085H1	887	1153	2	475178.1.oct	6131966H1	1	187
1	198450.6.oct	3451545H1	888	1141	2	475178.1.oct	4341985H1	1	306
1	198450.6.oct	2804083F6	896	1385	2	475178.1.oct	5696250H1	6	102
1	198450.6.oct	2804083H1	896	1154	2	475178.1.oct	g1577126	219	640
1	198450.6.oct	3519856H1	897	1223	2	475178.1.oct	5475396H1	224	472
1	198450.6.oct	2360526H1	911	1160	2	475178.1.oct	493554H1	246	491
1	198450.6.oct	g1489982	939	1229	2	475178.1.oct	493554R6	246	612
1	198450.6.oct	2585474H1	986	1236	2	475178.1.oct	265020H1	249	573
1	198450.6.oct	1385485H1	1017	1249	2	475178.1.oct	5871350H1	259	554
1	198450.6.oct	464838H1	1047	1254	2	475178.1.oct	g1886599	381	851
1	198450.6.oct	g4186989	1051	1479	2	475178.1.oct	5613813H1	383	475
1	198450.6.oct	g3932153	1055	1461	2	475178.1.oct	2518964H1	397	655
1	198450.6.oct	2519149H1	1055	1333	2	475178.1.oct	2518964F6	397	858
1	198450.6.oct	3326033H1	1076	1339	2	475178.1.oct	1533513H1	608	802
1	198450.6.oct	4383511H1	1114	1369	2	475178.1.oct	1533513F6	608	1058
1	198450.6.oct	6323272H1	1119	1395	2	475178.1.oct	g3742669	839	1335
1	198450.6.oct	2804083T6	1124	1676	2	475178.1.oct	g1337822	870	1335
1	198450.6.oct	g1367880	1160	1609	2	475178.1.oct	g3280761	876	1335
1	198450.6.oct	g4223520	1164	1461	2	475178.1.oct	g1337821	877	1347
1	198450.6.oct	2859754T6	1186	1698	2	475178.1.oct	g2883442	883	1311
1	198450.6.oct	758599H1	1223	1459	2	475178.1.oct	g2876528	895	1339
1	198450.6.oct	2614961T6	1274	1702	2	475178.1.oct	g1474211	1181	1336
1	198450.6.oct	g3755770	1280	1741	2	475178.1.oct	g3001396	1216	1278
1	198450.6.oct	g4390433	1284	1740	2	475178.1.oct	g2768096	1218	1281
1	198450.6.oct	g2540849	1290	1739	3	231793.2.oct	3406618H1	2148	2401
1	198450.6.oct	g1371334	1298	1739	3	231793.2.oct	1866779T7	2164	2565
1	198450.6.oct	g3721415	1300	1740	3	231793.2.oct	g3765637	2168	2622
1	198450.6.oct	5491460H1	1301	1434	3	231793.2.oct	5094942H1	2167	2412
1	198450.6.oct	6074015H1	1325	1579	3	231793.2.oct	3673817H1	1003	1285
1	198450.6.oct	g1443523	1326	1739	3	231793.2.oct	4580644H1	1173	1318
1	198450.6.oct	g3367015	1332	1745	3	231793.2.oct	g3049752	2237	2604

41	481454.4.dec	1206	1298	forward 3	SP
41	481454.4.dec	455	520	forward 2	SP
41	481454.4.dec	422	502	forward 2	SP
41	481454.4.d c	446	505	forward 2	SP
41	481454.4.dec	455	502	forward 2	SP
41	481454.4.dec	446	502	forward 2	SP
41	481454.4.dec	422	502	forward 2	SP
42	474800.7.dec	337	420	forward 1	SP
43	427883.13.dec	36	89	forward 3	TM
44	018945.1.dec	518	571	forward 2	TM
45	353271.2.dec	982	1062	forward 1	SP
46	221686.2.dec	728	793	forward 2	SP
46	221686.2.dec	728	781	forward 2	SP
46	221686.2.dec	728	799	forward 2	SP
47	233347.7.dec	972	1046	forward 3	SP
47	233347.7.dec	387	473	forward 3	SP
47	233347.7.dec	998	1069	forward 2	SP
47	233347.7.dec	998	1066	forward 2	SP
47	233347.7.dec	228	326	forward 3	SP
47	233347.7.dec	273	335	forward 3	TM
47	233347.7.dec	998	1051	forward 2	SP
47	233347.7.dec	264	317	forward 3	TM
47	233347.7.dec	264	323	forward 3	TM
47	233347.7.dec	273	338	forward 3	TM
47	233347.7.dec	273	344	forward 3	TM
47	233347.7.dec	264	326	forward 3	SP
47	233347.7.dec	264	335	forward 3	SP
48	230631.3.dec	1675	1737	forward 1	TM
48	230631.3.dec	524	577	forward 2	SP
48	230631.3.dec	524	574	forward 2	SP
48	230631.3.dec	1675	1734	forward 1	TM
49	335146.1.dec	218	271	forward 2	TM
49	335146.1.dec	203	268	forward 2	TM
49	335146.1.dec	218	274	forward 2	TM
50	337160.1.dec	281	385	forward 2	SP
51	346341.12.dec	1434	1520	forward 3	SP
51	346341.12.dec	2589	2654	forward 3	SP
51	346341.12.dec	1208	1291	forward 2	SP
51	346341.12.dec	2589	2660	forward 3	SP
51	346341.12.dec	2589	2648	forward 3	SP
51	346341.12.dec	2517	2591	forward 3	TM
51	346341.12.dec	3712	3762	forward 1	TM
51	346341.12.dec	2589	2642	forward 3	SP
51	346341.12.dec	982	1068	forward 1	SP
51	346341.12.dec	3712	3768	forward 1	TM
52	428745.2.dec	113	181	forward 2	SP
53	444839.17.dec	265	312	forward 1	TM
54	245000.6.dec	797	868	forward 2	TM
54	245000.6.dec	806	868	forward 2	SP
54	245000.6.dec	806	874	forward 2	SP
54	245000.6.dec	251	367	forward 2	SP
54	245000.6.dec	563	619	forward 2	SP
54	245000.6.dec	572	634	forward 2	TM
54	245000.6.dec	806	865	forward 2	TM
54	245000.6.dec	767	841	forward 2	SP
54	245000.6.dec	812	865	forward 2	TM
54	245000.6.dec	806	850	forward 2	SP
54	245000.6.dec	773	862	forward 2	SP
54	245000.6.dec	806	862	forward 2	SP
55	428362.36.dec	270	326	forward 3	TM
56	480710.12.dec	878	931	forward 2	TM
56	480710.12.dec	2216	2266	forward 2	TM
56	480710.12.dec	22	126	forward 1	SP
57	234137.10.dec	548	646	forward 2	SP
58	480630.4.dec	881	931	forward 2	TM
59	480951.5.d c	964	1023	forward 1	SP

Table 1 cont.

59	480951.5.dec	964	1011	forward 1	SP
59	480951.5.dec	1479	1538	forward 3	TM
60	350399.5.dec	1080	1127	forward 3	SP
60	350399.5.dec	1697	1759	forward 2	TM
60	350399.5.dec	3742	3801	forward 1	SP
60	350399.5.dec	1856	1918	forward 2	TM
60	350399.5.dec	1703	1750	forward 2	TM
60	350399.5.dec	2169	2234	forward 3	SP
60	350399.5.dec	2183	2239	forward 2	TM
60	350399.5.dec	2169	2228	forward 3	TM
60	350399.5.dec	1173	1223	forward 3	TM
60	350399.5.dec	1709	1765	forward 2	TM
60	350399.5.dec	3751	3804	forward 1	TM
60	350399.5.dec	1697	1768	forward 2	TM
61	085713.2.dec	2469	2528	forward 3	SP
61	085713.2.dec	1792	1848	forward 1	SP
61	085713.2.dec	2481	2540	forward 3	TM
61	085713.2.dec	2447	2500	forward 2	TM
61	085713.2.dec	2456	2527	forward 2	TM
61	085713.2.dec	2456	2518	forward 2	TM
61	085713.2.dec	2344	2400	forward 1	SP
61	085713.2.dec	2464	2523	forward 1	TM
61	085713.2.dec	125	175	forward 2	SP
61	085713.2.dec	2456	2512	forward 2	TM
61	085713.2.dec	2458	2511	forward 1	TM
61	085713.2.dec	2540	2596	forward 2	SP
62	245014.1.dec	791	865	forward 2	SP
62	245014.1.dec	770	823	forward 2	TM
62	245014.1.dec	785	850	forward 2	TM
62	245014.1.dec	785	856	forward 2	TM
63	117464.7.dec	1411	1458	forward 1	SP
63	117464.7.dec	1399	1473	forward 1	SP
63	117464.7.dec	1408	1470	forward 1	SP
63	117464.7.dec	1921	1983	forward 1	SP
63	117464.7.dec	231	278	forward 3	SP
63	117464.7.dec	574	633	forward 1	SP
63	117464.7.dec	1909	1992	forward 1	SP
63	117464.7.dec	1664	1720	forward 2	TM
63	117464.7.dec	1939	1992	forward 1	SP
63	117464.7.dec	2975	3040	forward 2	SP
63	117464.7.dec	2740	2808	forward 1	SP
63	117464.7.dec	2966	3052	forward 2	SP
63	117464.7.dec	1906	1983	forward 1	TM
63	117464.7.dec	1918	1968	forward 1	SP
63	117464.7.dec	1930	1989	forward 1	TM
63	117464.7.dec	1918	1986	forward 1	SP
63	117464.7.dec	1921	1992	forward 1	SP
63	117464.7.dec	231	302	forward 3	SP
63	117464.7.dec	1423	1494	forward 1	TM
63	117464.7.dec	1933	1983	forward 1	TM
63	117464.7.dec	1933	1995	forward 1	TM

Table 2 cont.

4	000010.4.oct	4984706H1	1140	1346	4	000010.4.oct	3165805H1	920	1199
4	000010.4.oct	4594569H1	1142	1396	4	000010.4.oct	3165853H1	920	1196
4	000010.4.oct	3045057H1	1147	1434	4	000010.4.oct	4729385H1	924	1181
4	000010.4.oct	1401088H1	1166	1403	4	000010.4.oct	6298177H1	937	1259
4	000010.4.oct	3552750H1	1172	1391	4	000010.4.oct	4398053H1	989	1244
4	000010.4.oct	912266H1	1180	1310	4	000010.4.oct	4399305H1	988	1259
4	000010.4.oct	1850668T6	1179	1772	4	000010.4.oct	3600193H1	991	1273
4	000010.4.oct	1326577H1	1209	1470	4	000010.4.oct	4218371H1	991	1165
4	000010.4.oct	1323667H1	1209	1430	4	000010.4.oct	2533935F6	1	130
4	000010.4.oct	984923R1	1211	1664	4	000010.4.oct	2533935H1	1	212
4	000010.4.oct	984923H1	1211	1418	4	000010.4.oct	g2205347	30	247
4	000010.4.oct	1261381T6	1223	1769	4	000010.4.oct	2497994F6	30	424
4	000010.4.oct	3818091H1	1225	1478	4	000010.4.oct	5870230H1	28	141
4	000010.4.oct	3819406H1	1225	1495	4	000010.4.oct	g2205289	30	267
4	000010.4.oct	3415179H1	1228	1481	4	000010.4.oct	2497994H1	30	145
4	000010.4.oct	g1489942	1228	1599	4	000010.4.oct	g2002304	30	306
4	000010.4.oct	4357827H1	1234	1489	4	000010.4.oct	149399H1	42	206
4	000010.4.oct	3816557H1	1236	1530	4	000010.4.oct	4421431H1	45	243
4	000010.4.oct	g1549922	1252	1602	4	000010.4.oct	5086835H1	59	109
4	000010.4.oct	1960790T6	1276	1765	4	000010.4.oct	3798389H1	74	336
4	000010.4.oct	5621050H1	1288	1573	4	000010.4.oct	2502489F6	79	482
4	000010.4.oct	2502489T6	1294	1765	4	000010.4.oct	2502489H1	79	294
4	000010.4.oct	4297766H1	1294	1506	4	000010.4.oct	3347907H1	95	324
4	000010.4.oct	4298064H1	1294	1534	4	000010.4.oct	1418374H1	95	240
4	000010.4.oct	1843689H1	1305	1561	4	000010.4.oct	g2002139	99	536
4	000010.4.oct	g518355	1307	1808	4	000010.4.oct	2096696H1	106	351
4	000010.4.oct	2557004H2	274	386	4	000010.4.oct	4911182H1	109	403
4	000010.4.oct	2557066H1	274	518	4	000010.4.oct	1003086H1	114	343
4	000010.4.oct	1816539H1	275	524	4	000010.4.oct	3321596H2	128	373
4	000010.4.oct	3758495H1	283	493	4	000010.4.oct	3878602H1	129	434
4	000010.4.oct	1960790R6	290	364	4	000010.4.oct	3740635H1	129	320
4	000010.4.oct	1960790H1	290	509	4	000010.4.oct	4042307H1	105	163
4	000010.4.oct	2703769H1	314	572	4	000010.4.oct	2587619H1	131	379
4	000010.4.oct	2193493H1	316	571	4	000010.4.oct	2584021H1	131	377
4	000010.4.oct	2878946H1	350	628	4	000010.4.oct	2080578H1	133	385
4	000010.4.oct	3674909H1	369	637	4	000010.4.oct	g2410855	145	374
4	000010.4.oct	3957836H2	370	628	4	000010.4.oct	4832261H1	154	326
4	000010.4.oct	3674529H1	370	613	4	000010.4.oct	2226661H1	158	368
4	000010.4.oct	5396777H1	385	647	4	000010.4.oct	996378H1	180	477
4	000010.4.oct	4729679H1	389	662	4	000010.4.oct	3599007H1	181	482
4	000010.4.oct	1232381H1	412	649	4	000010.4.oct	4635262H1	204	450
4	000010.4.oct	2359821H1	418	655	4	000010.4.oct	2716023H1	214	448
4	000010.4.oct	5295590H1	446	716	4	000010.4.oct	3472595H1	232	414
4	000010.4.oct	4667072H1	488	720	4	000010.4.oct	2557058H1	274	523
4	000010.4.oct	2919365H1	528	796	4	000010.4.oct	2497994T6	1577	1762
4	000010.4.oct	5378869H1	547	753	4	000010.4.oct	4127359H1	1588	1807
4	000010.4.oct	5398383H1	561	796	4	000010.4.oct	g2444595	1594	1809
4	000010.4.oct	3254113H1	589	859	4	000010.4.oct	g2324424	1594	1808
4	000010.4.oct	4761817H1	592	869	4	000010.4.oct	g2324565	1594	1808
4	000010.4.oct	1257093F1	599	1194	4	000010.4.oct	4855237H1	1607	1802
4	000010.4.oct	1257093H1	599	834	4	000010.4.oct	4768170H1	1622	1808
4	000010.4.oct	4984849H1	601	874	4	000010.4.oct	4769968H1	1622	1808
4	000010.4.oct	1850668H1	607	913	4	000010.4.oct	g3133564	1623	1808
4	000010.4.oct	1259277H1	619	861	4	000010.4.oct	5152534H1	1640	1899
4	000010.4.oct	488977H1	625	876	4	000010.4.oct	2533935T6	1677	1766
4	000010.4.oct	5173650H1	632	859	4	000010.4.oct	940189H1	1690	1808
4	000010.4.oct	3990710H1	658	961	4	000010.4.oct	2636973H1	1691	1799
4	000010.4.oct	5072810H1	674	925	4	000010.4.oct	2553110H1	1743	1808
4	000010.4.oct	2995522H1	772	1042	4	000010.4.oct	5002788H1	1752	1808
4	000010.4.oct	4418859H1	781	1037	4	000010.4.oct	5106690H1	1756	1808
4	000010.4.oct	4339619H1	857	1096	4	000010.4.oct	3630725H1	1556	1737
4	000010.4.oct	3207980H1	881	991	4	000010.4.oct	2570529H1	1556	1780
4	000010.4.oct	1261381R1	888	1312	4	000010.4.oct	g1717016	1562	1808
4	000010.4.oct	1261381H1	888	1134	5	412959.6.oct	5216131H1	393	673
4	000010.4.oct	1261381R6	888	1341	5	412959.6.oct	5282328H2	399	649
4	000010.4.oct	5714423H1	892	1195	5	412959.6.oct	1286604H1	401	654
4	000010.4.oct	447362H1	900	1120	5	412959.6.oct	5075560H1	403	678
4	000010.4. ct	5265158H1	904	1130	5	412959.6.oct	g4306032	416	815

Table 2 cont.

3	231793.2.oct	1707686T6	2245	2557
3	231793.2.oct	5048501H1	2256	2540
3	231793.2.oct	2673033T6	2271	2565
3	231793.2.oct	g2556740	2285	2602
3	231793.2.oct	g4078219	2330	2626
3	231793.2.oct	2883970T6	2365	2585
3	231793.2.oct	3512992H1	2365	2563
3	231793.2.oct	3743582H1	1	299
3	231793.2.oct	3490362H1	3	199
3	231793.2.oct	6301123H1	10	295
3	231793.2.oct	2488457H1	1176	1404
3	231793.2.oct	2623858R6	1183	1496
3	231793.2.oct	2623858H1	1183	1432
3	231793.2.oct	4650753H1	1347	1490
3	231793.2.oct	2793766H1	1364	1658
3	231793.2.oct	1803565H1	1548	1827
3	231793.2.oct	6173678H1	1561	1850
3	231793.2.oct	1214293T6	2183	2564
3	231793.2.oct	1214293R6	2184	2577
3	231793.2.oct	1214293H1	2194	2407
3	231793.2.oct	1803565T6	2104	2547
3	231793.2.oct	1001126T6	2092	2558
3	231793.2.oct	4170673H1	2146	2407
3	231793.2.oct	5027277H1	1995	2261
3	231793.2.oct	3803405H1	2038	2335
3	231793.2.oct	5095560H1	2046	2221
3	231793.2.oct	4213438H1	2072	2273
3	231793.2.oct	1986603T6	2084	2560
3	231793.2.oct	g1979679	1896	2192
3	231793.2.oct	4593321H1	1918	2189
3	231793.2.oct	5986230H1	1917	2189
3	231793.2.oct	g2277027	1948	2321
3	231793.2.oct	6171737H1	1955	2242
3	231793.2.oct	5951283H1	1974	2290
3	231793.2.oct	2673033F6	1982	2501
3	231793.2.oct	2673033H1	1982	2213
3	231793.2.oct	977810H1	1989	2200
3	231793.2.oct	5281570H2	1570	1837
3	231793.2.oct	4731704H1	1573	1859
3	231793.2.oct	158289R1	1649	2082
3	231793.2.oct	158289H1	1650	1825
3	231793.2.oct	4598887H1	1664	1901
3	231793.2.oct	3559656H1	1702	1994
3	231793.2.oct	3961916H1	1703	1835
3	231793.2.oct	3695880H1	1755	2042
3	231793.2.oct	4048712H1	1815	2092
3	231793.2.oct	1707686H1	1884	2072
3	231793.2.oct	5296093H1	1892	2102
3	231793.2.oct	g2322181	2439	2604
3	231793.2.oct	1302067T7	2444	2562
3	231793.2.oct	1302517F6	2451	2602
3	231793.2.oct	1302517H1	2451	2602
3	231793.2.oct	134723H1	2466	2602
3	231793.2.oct	g1195715	2560	2610
3	231793.2.oct	1986603R6	863	1385
3	231793.2.oct	1991005H1	915	1072
3	231793.2.oct	3962341H1	968	1258
3	231793.2.oct	1001126R6	324	881
3	231793.2.oct	4049712H1	367	637
3	231793.2.oct	3767101H1	532	647
3	231793.2.oct	2791795H1	508	797
3	231793.2.oct	4576054H1	561	820
3	231793.2.oct	5593839H1	731	990
3	231793.2.oct	5052279H1	833	967
3	231793.2. ct	1986603H1	863	1144
3	231793.2.oct	1214167H1	2195	2439
3	231793.2.oct	5084768H1	2222	2437
3	231793.2.oct	g2347914	2221	2601
3	231793.2.oct	1914969H1	2225	2477
3	231793.2.oct	3355002H1	21	302
3	231793.2.oct	1522723H1	22	216
3	231793.2.oct	2790244H2	30	335
3	231793.2.oct	1866779F6	33	411
3	231793.2.oct	1866779H1	33	313
3	231793.2.oct	1311083H1	80	298
3	231793.2.oct	3236153H1	111	358
3	231793.2.oct	5158979H1	202	425
3	231793.2.oct	1390306H1	287	537
3	231793.2.oct	1390212H1	287	443
4	000010.4.oct	3254213T6	1335	1763
4	000010.4.oct	1370046H1	1337	1486
4	000010.4.oct	5396777T1	1343	1771
4	000010.4.oct	1370046R6	1342	1707
4	000010.4.oct	1370103H1	1342	1584
4	000010.4.oct	1726162F6	1349	1799
4	000010.4.oct	5372922H1	1349	1573
4	000010.4.oct	1726162H1	1349	1549
4	000010.4.oct	1726162T6	1350	1770
4	000010.4.oct	g2903534	1351	1580
4	000010.4.oct	g3645063	1355	1808
4	000010.4.oct	2499364T6	1364	1770
4	000010.4.oct	g3051966	1379	1808
4	000010.4.oct	g1489943	1390	1808
4	000010.4.oct	5085122H1	1389	1642
4	000010.4.oct	g4018720	1393	1810
4	000010.4.oct	g4069319	1396	1809
4	000010.4.oct	g4190861	1400	1812
4	000010.4.oct	g3307421	1406	1817
4	000010.4.oct	g2206554	1408	1809
4	000010.4.oct	1654556H1	1415	1631
4	000010.4.oct	g2876054	1416	1580
4	000010.4.oct	g4533961	1419	1809
4	000010.4.oct	g2727372	1423	1580
4	000010.4.oct	5327974H1	1429	1672
4	000010.4.oct	4321986H1	1430	1690
4	000010.4.oct	1459590R1	1435	1808
4	000010.4.oct	g1940736	1441	1811
4	000010.4.oct	5406569H1	1456	1636
4	000010.4.oct	g615220	1477	1808
4	000010.4.oct	g778928	1487	1807
4	000010.4.oct	6096110H1	1495	1807
4	000010.4.oct	g3736024	1496	1809
4	000010.4.oct	g2753028	1500	1580
4	000010.4.oct	956928H1	1512	1803
4	000010.4.oct	g1551537	1513	1808
4	000010.4.oct	956928T1	1512	1769
4	000010.4.oct	g821709	1522	1833
4	000010.4.oct	g2100454	1521	1808
4	000010.4.oct	4725870H1	1537	1781
4	000010.4.oct	3786249H1	1544	1808
4	000010.4.oct	4218279H1	991	1233
4	000010.4.oct	5439541H1	1006	1066
4	000010.4.oct	5439514H1	1006	1242
4	000010.4.oct	4863426H1	1011	1294
4	000010.4.oct	3882069H1	1038	1277
4	000010.4.oct	2963213H1	1058	1361
4	000010.4.oct	6379351H1	1064	1333
4	000010.4.oct	g1928730	1068	1409
4	000010.4.oct	g1717071	1069	1257
4	000010.4.oct	439860H1	1080	1212
4	000010.4.oct	4645642H1	1097	1370
4	000010.4.oct	1315140H1	1110	1358
4	000010.4.oct	3152664H1	1110	1402
4	000010.4.oct	4858515H1	1122	1353
4	000010.4.oct	1459590H1	1124	1376
4	000010.4.oct	4292624H1	1134	1395

Table 2 cont.

5	412959.6.oct	g2265153	614	967	6	331521.5.oct	g3736851	1121	1507
5	412959.6.oct	g1745215	619	815	6	331521.5.oct	5598577H1	1123	1315
5	412959.6.oct	g2368862	627	815	6	331521.5.oct	g2270261	1138	1501
5	412959.6.oct	g2703493	628	970	6	331521.5.oct	927617T6	1142	1460
5	412959.6.oct	g1493098	628	982	6	331521.5.oct	g922764	1144	1480
5	412959.6.oct	g3040120	630	978	6	331521.5.oct	g922061	1150	1496
5	412959.6.oct	g2575651	631	815	6	331521.5.oct	g3417656	1150	1498
5	412959.6.oct	g1618594	642	971	6	331521.5.oct	g3745245	1150	1498
5	412959.6.oct	g1148550	649	885	6	331521.5.oct	3943483H1	1035	1301
5	412959.6.oct	2821589H1	656	959	6	331521.5.oct	1787637H1	1041	1273
5	412959.6.oct	g1218727	682	961	6	331521.5.oct	838819H1	634	888
5	412959.6.oct	g787387	692	967	6	331521.5.oct	g1187465	664	913
5	412959.6.oct	1695326H1	691	815	6	331521.5.oct	4667001H1	692	967
5	412959.6.oct	g2177825	702	967	6	331521.5.oct	3113662H1	509	730
5	412959.6.oct	2725050H1	718	815	6	331521.5.oct	g1986323	509	821
5	412959.6.oct	2674048T6	758	933	6	331521.5.oct	2732541H1	516	739
5	412959.6.oct	g1860722	764	1003	6	331521.5.oct	g1239894	558	772
5	412959.6.oct	g1139057	773	982	6	331521.5.oct	3513041H1	557	799
5	412959.6.oct	g3145267	794	949	6	331521.5.oct	3190732H1	607	963
5	412959.6.oct	g1265363	803	975	6	331521.5.oct	2375477H1	505	725
5	412959.6.oct	4771510H1	819	989	6	331521.5.oct	3149260H1	506	788
5	412959.6.oct	778431H1	825	981	6	331521.5.oct	g3595860	1088	1498
5	412959.6.oct	g3149926	832	885	6	331521.5.oct	g3146187	1099	1501
5	412959.6.oct	g3043195	849	970	6	331521.5.oct	4979280H1	1109	1373
6	331521.5.oct	2211724H1	478	739	6	331521.5.oct	g3250147	1114	1505
6	331521.5.oct	3456836H1	480	709	6	331521.5.oct	g3431781	1118	1499
6	331521.5.oct	2202654H1	485	720	6	331521.5.oct	3629028H1	1044	1329
6	331521.5.oct	2661126T6	968	1458	6	331521.5.oct	g3404876	1057	1501
6	331521.5.oct	g3872415	1033	1498	6	331521.5.oct	3444045H1	1058	1315
6	331521.5.oct	3943483F6	1035	1499	6	331521.5.oct	1212854T6	1084	1475
6	331521.5.oct	g3884652	1157	1503	6	331521.5.oct	5994615H1	491	790
6	331521.5.oct	g1197983	1173	1502	6	331521.5.oct	5574629H1	492	750
6	331521.5.oct	4666217T6	896	1475	6	331521.5.oct	3091023H1	490	777
6	331521.5.oct	4378681H1	920	1191	6	331521.5.oct	077179H1	491	690
6	331521.5.oct	5563982H1	951	1165	6	331521.5.oct	422847H1	495	777
6	331521.5.oct	4666217F6	891	1066	6	331521.5.oct	g2224124	1204	1502
6	331521.5.oct	4666217H1	891	1158	6	331521.5.oct	g2238189	1216	1516
6	331521.5.oct	g3801327	1271	1499	6	331521.5.oct	5730657H1	1233	1488
6	331521.5.oct	g2411273	1285	1501	6	331521.5.oct	3510032T7	1237	1459
6	331521.5.oct	g566119	1304	1497	6	331521.5.oct	g2882731	1242	1503
6	331521.5.oct	6092081H1	1329	1498	6	331521.5.oct	g570486	1	181
6	331521.5.oct	853544H1	1352	1485	6	331521.5.oct	g875762	2	309
6	331521.5.oct	2705657T6	1353	1457	6	331521.5.oct	g831148	2	358
6	331521.5.oct	2705657H1	1360	1498	6	331521.5.oct	4175396H1	494	777
6	331521.5.oct	2705657F6	1360	1498	6	331521.5.oct	4123843H1	499	635
6	331521.5.oct	g868758	1416	1505	6	331521.5.oct	781855R1	498	1067
6	331521.5.oct	g907918	1444	1499	6	331521.5.oct	781855H1	498	742
6	331521.5.oct	1212854H1	718	1014	6	331521.5.oct	g1281868	504	951
6	331521.5.oct	5097150H1	718	983	6	331521.5.oct	5463846H1	497	689
6	331521.5.oct	2005993H1	718	889	6	331521.5.oct	5120226H1	506	790
6	331521.5.oct	5114952H1	727	996	6	331521.5.oct	g830914	1182	1505
6	331521.5.oct	4032072H1	780	1019	6	331521.5.oct	g1486742	1197	1517
6	331521.5.oct	2046722H1	445	722	6	331521.5.oct	g4296634	1200	1504
6	331521.5.oct	6436791H1	451	976	7	902114.1.oct	3815354H1	1	277
6	331521.5.oct	2507802H1	475	713	7	902114.1.oct	6099860H1	3	269
6	331521.5.oct	3673647H1	431	736	7	902114.1.oct	g3419125	193	601
6	331521.5.oct	g922133	444	781	7	902114.1.oct	1869318H1	205	458
6	331521.5.oct	g922831	441	726	7	902114.1.oct	g3434169	236	599
6	331521.5.oct	3510032F6	255	827	7	902114.1.oct	g2211756	313	614
6	331521.5.oct	3510032H1	255	561	7	902114.1.oct	4664818H1	395	644
6	331521.5.oct	3115530H1	435	730	7	902114.1.oct	934433R1	476	921
6	331521.5.oct	2579471H1	427	706	7	902114.1.oct	934433H1	476	752
6	331521.5.oct	g1156421	709	861	7	902114.1.oct	2848096H1	725	985
6	331521.5.oct	g875763	1152	1505	8	481382.1.oct	4140109H1	35	204
6	331521.5.oct	g2279775	1153	1499	8	481382.1.oct	3793754H1	35	189
6	331521.5.oct	g1158127	1154	1503	8	481382.1.oct	2769459H1	35	116
6	331521.5.oct	g4147609	1155	1499	8	481382.1.oct	1732095T6	35	237
6	331521.5.oct	g2240963	1118	1498	8	481382.1.oct	1732095H1	84	358

Table 2 cont.

5	412959.6.oct	2470746H1	416	614
5	412959.6.oct	5353589T6	422	966
5	412959.6.oct	g4189438	430	815
5	412959.6.oct	g4188920	430	815
5	412959.6.oct	g4188326	437	815
5	412959.6.oct	g4302701	439	815
5	412959.6.oct	g3539347	444	815
5	412959.6.oct	776186H1	445	673
5	412959.6.oct	g3048416	448	815
5	412959.6.oct	g2782788	447	815
5	412959.6.oct	g2901391	464	815
5	412959.6.oct	g3801539	471	815
5	412959.6.oct	g2874031	480	889
5	412959.6.oct	g2741857	489	979
5	412959.6.oct	g2675057	493	815
5	412959.6.oct	g3038152	493	970
5	412959.6.oct	g1639027	501	715
5	412959.6.oct	g4373288	506	973
5	412959.6.oct	g3988957	509	815
5	412959.6.oct	g3961978	522	815
5	412959.6.oct	g3869490	525	968
5	412959.6.oct	g4004707	525	977
5	412959.6.oct	g3086363	530	815
5	412959.6.oct	g3897838	533	967
5	412959.6.oct	g2115818	534	973
5	412959.6.oct	g3281206	537	970
5	412959.6.oct	g4070114	540	971
5	412959.6.oct	g4069838	543	980
5	412959.6.oct	g2934294	545	982
5	412959.6.oct	g1331787	545	973
5	412959.6.oct	g2526614	546	976
5	412959.6.oct	g2932297	548	974
5	412959.6.oct	5608040H1	558	805
5	412959.6.oct	g2264793	563	967
5	412959.6.oct	g3281079	573	973
5	412959.6.oct	2672133H1	581	814
5	412959.6.oct	1772941H1	581	855
5	412959.6.oct	g3038159	584	970
5	412959.6.oct	g3958916	591	976
5	412959.6.oct	g2876891	597	970
5	412959.6.oct	g1741463	597	949
5	412959.6.oct	g1882898	598	967
5	412959.6.oct	4624368H1	3	240
5	412959.6.oct	2654578H1	3	303
5	412959.6.oct	4460844H1	4	197
5	412959.6.oct	2644911H1	4	269
5	412959.6.oct	g2159460	4	460
5	412959.6.oct	4065681H1	4	276
5	412959.6.oct	686032H1	7	225
5	412959.6.oct	3988406H1	7	195
5	412959.6.oct	041056H1	9	275
5	412959.6.oct	g1745820	11	208
5	412959.6.oct	4154075H1	6	257
5	412959.6.oct	3156341H1	10	285
5	412959.6.oct	2551586H1	10	255
5	412959.6.oct	g1996909	10	311
5	412959.6.oct	034375H1	12	226
5	412959.6.oct	g1618697	13	306
5	412959.6.oct	5374474H1	13	185
5	412959.6.oct	5152582H1	14	277
5	412959.6.oct	5069232H1	14	271
5	412959.6.oct	3706309H1	7	290
5	412959.6.oct	1333267H1	14	298
5	412959.6.oct	2764864H1	14	255
5	412959.6.oct	4888767H1	14	282
5	412959.6.oct	3479540H1	14	247
5	412959.6.oct	2912750H1	14	286
5	412959.6.oct	4295435H1	14	234
5	412959.6.oct	2763336H1	14	249
5	412959.6.oct	1703741H1	7	225
5	412959.6.oct	1632693H1	14	225
5	412959.6.oct	4296049H1	14	268
5	412959.6.oct	5074132H1	14	297
5	412959.6.oct	2599392H1	1	268
5	412959.6.oct	3846287H1	2	234
5	412959.6.oct	g1157175	1	358
5	412959.6.oct	1253994H1	1	212
5	412959.6.oct	4527929H1	1	264
5	412959.6.oct	g2029372	1	177
5	412959.6.oct	775186H1	2	217
5	412959.6.oct	5353589F6	2	480
5	412959.6.oct	2586285H1	1	218
5	412959.6.oct	3206555H1	2	177
5	412959.6.oct	3269334H1	3	233
5	412959.6.oct	3495588H1	14	298
5	412959.6.oct	4655833H1	16	264
5	412959.6.oct	496681H1	23	259
5	412959.6.oct	3679041H1	26	206
5	412959.6.oct	496697H1	23	248
5	412959.6.oct	5209034H1	27	292
5	412959.6.oct	6110991H1	29	247
5	412959.6.oct	g1745450	29	322
5	412959.6.oct	3879459H1	35	312
5	412959.6.oct	3752872H1	39	255
5	412959.6.oct	4756963H1	59	311
5	412959.6.oct	5644885H1	60	188
5	412959.6.oct	g1940430	73	532
5	412959.6.oct	2904488H1	130	412
5	412959.6.oct	g1987165	144	469
5	412959.6.oct	g1237710	146	287
5	412959.6.oct	2120694H1	166	337
5	412959.6.oct	3081510H1	165	470
5	412959.6.oct	g786906	173	499
5	412959.6.oct	981383H1	191	432
5	412959.6.oct	3705428H1	201	468
5	412959.6.oct	g1745306	206	502
5	412959.6.oct	g1981799	245	508
5	412959.6.oct	2581258H1	339	583
5	412959.6.oct	5909478H1	340	621
5	412959.6.oct	1781527T6	346	929
5	412959.6.oct	4129041H1	348	631
5	412959.6.oct	5029110H1	347	611
5	412959.6.oct	3771103H1	357	530
5	412959.6.oct	1781527H1	360	619
5	412959.6.oct	1781527R6	360	826
5	412959.6.oct	3029101T6	372	931
5	412959.6.oct	2956192H1	372	645
5	412959.6.oct	g1319510	377	893
5	412959.6.oct	g1447775	254	598
5	412959.6.oct	g1882897	259	612
5	412959.6.oct	g828247	261	526
5	412959.6.oct	2350937H1	272	467
5	412959.6.oct	1307384H1	275	507
5	412959.6.oct	1541305H1	288	497
5	412959.6.oct	4744668H1	392	660
5	412959.6.oct	5435925H1	300	532
5	412959.6.oct	g2838960	866	972
5	412959.6.oct	g1745821	866	967
5	412959.6.oct	721875H1	866	958
5	412959.6.oct	721352H1	866	958
5	412959.6.oct	g3041378	866	970
5	412959.6.oct	g1193527	907	979
5	412959.6.oct	g2185358	599	971
5	412959.6.oct	g3785891	609	995
5	412959.6.oct	g3015900	610	970
5	412959.6.oct	1918481H1	614	815

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9	903849.1.oct	6260688H1	1026	1267	9	903849.1.oct	4245542H1	257	502
9	903849.1.oct	1613848H1	1028	1243	9	903849.1.oct	1450643F1	73	498
9	903849.1.oct	4157804T8	1035	1591	9	903849.1.oct	4245904H1	257	517
9	903849.1.oct	6190485H1	1034	1319	9	903849.1.oct	1450643H1	73	332
9	903849.1.oct	4550411T1	1047	1573	9	903849.1.oct	5698478H1	77	265
9	903849.1.oct	2173189T6	1048	1572	9	903849.1.oct	2539842H1	87	329
9	903849.1.oct	4549428T1	1061	1555	9	903849.1.oct	5065835H1	103	348
9	903849.1.oct	748919H1	1074	1310	9	903849.1.oct	5377044H1	131	394
9	903849.1.oct	748919R1	1074	1611	9	903849.1.oct	3689228H1	292	570
9	903849.1.oct	2700820H1	1083	1352	9	903849.1.oct	g1276068	313	801
9	903849.1.oct	1709866H1	1095	1321	9	903849.1.oct	3479853H1	321	651
9	903849.1.oct	1709866F6	1095	1473	9	903849.1.oct	2951083H1	330	589
9	903849.1.oct	2350024H1	1097	1310	9	903849.1.oct	955261R1	334	807
9	903849.1.oct	2719920H1	1101	1354	9	903849.1.oct	955261H1	334	615
9	903849.1.oct	2720624H1	1101	1335	9	903849.1.oct	3234424H1	345	517
9	903849.1.oct	3051469H1	1108	1388	9	903849.1.oct	264620H1	358	701
9	903849.1.oct	3050747H1	1108	1446	9	903849.1.oct	2344474F6	369	815
9	903849.1.oct	1870888T6	1119	1571	9	903849.1.oct	2344474H1	369	537
9	903849.1.oct	1255114T6	1124	1569	9	903849.1.oct	3684753H1	378	693
9	903849.1.oct	g2575208	1135	1619	9	903849.1.oct	3777349H1	390	672
9	903849.1.oct	g3151314	1139	1616	9	903849.1.oct	2636983H1	398	638
9	903849.1.oct	g1018704	1142	1413	9	903849.1.oct	3969738H1	403	689
9	903849.1.oct	1709866T6	1148	1579	9	903849.1.oct	3720303H1	408	700
9	903849.1.oct	g2837554	1150	1614	9	903849.1.oct	4616163H1	414	680
9	903849.1.oct	g1801648	1	220	9	903849.1.oct	1610601H1	417	655
9	903849.1.oct	4768624H1	1	267	9	903849.1.oct	1610601F6	417	797
9	903849.1.oct	3693504H1	1	307	9	903849.1.oct	4325728H1	419	601
9	903849.1.oct	3693519H1	1	301	9	903849.1.oct	3660219H1	422	641
9	903849.1.oct	4160192H1	3	250	9	903849.1.oct	4542103H1	422	675
9	903849.1.oct	3617693H1	3	278	9	903849.1.oct	5210061H1	430	660
9	903849.1.oct	3617093H1	3	254	9	903849.1.oct	1418988H1	431	673
9	903849.1.oct	3651125H1	6	290	9	903849.1.oct	972888H1	431	668
9	903849.1.oct	3381741H1	14	247	9	903849.1.oct	3202649H1	438	664
9	903849.1.oct	4527453H1	16	93	9	903849.1.oct	4637919H1	451	714
9	903849.1.oct	4084909H1	16	192	9	903849.1.oct	3415427H1	464	722
9	903849.1.oct	491926H1	16	197	9	903849.1.oct	4093051H1	477	743
9	903849.1.oct	3792824H1	17	282	9	903849.1.oct	5734663H1	495	746
9	903849.1.oct	3743920H1	18	321	9	903849.1.oct	g944573	510	854
9	903849.1.oct	3460060H1	17	276	9	903849.1.oct	g1694097	515	846
9	903849.1.oct	4527596H1	23	270	9	903849.1.oct	g751975	522	768
9	903849.1.oct	3686573H1	19	317	9	903849.1.oct	000134H1	527	983
9	903849.1.oct	2173189F6	20	94	9	903849.1.oct	5207738H1	530	767
9	903849.1.oct	2549457H1	18	270	9	903849.1.oct	3092084H1	540	805
9	903849.1.oct	6384945H1	20	324	9	903849.1.oct	3092084F6	541	982
9	903849.1.oct	2173189H1	20	251	9	903849.1.oct	3877454H1	548	825
9	903849.1.oct	3510073H1	23	294	9	903849.1.oct	4441451H1	549	794
9	903849.1.oct	3225307H1	23	316	9	903849.1.oct	g920316	589	863
9	903849.1.oct	1870888F6	23	547	9	903849.1.oct	1527791H1	44	242
9	903849.1.oct	1870888H1	23	287	9	903849.1.oct	3074436H1	44	308
9	903849.1.oct	3075151H1	23	317	9	903849.1.oct	g831292	26	423
9	903849.1.oct	2720653H1	23	277	9	903849.1.oct	g1291703	27	510
9	903849.1.oct	3507839H1	24	313	9	903849.1.oct	g573100	36	337
9	903849.1.oct	5842380H1	26	91	9	903849.1.oct	1824463H1	35	263
9	903849.1.oct	1870853H1	25	251	9	903849.1.oct	5117411H1	39	298
9	903849.1.oct	4552316H1	24	172	9	903849.1.oct	4984956H1	36	288
9	903849.1.oct	3742953H1	25	324	9	903849.1.oct	483920H1	40	265
9	903849.1.oct	5276481H1	208	377	9	903849.1.oct	4154493H1	41	292
9	903849.1.oct	3284445H1	62	308	9	903849.1.oct	g1274878	43	654
9	903849.1.oct	2108887H1	211	353	9	903849.1.oct	2768516H1	41	302
9	903849.1.oct	2475835H1	63	284	9	903849.1.oct	1460203H1	41	273
9	903849.1.oct	3029734H1	65	343	9	903849.1.oct	g1271819	44	331
9	903849.1.oct	g1959086	65	486	9	903849.1.oct	2259610H1	42	249
9	903849.1.oct	3289141H1	214	445	9	903849.1.oct	3692010H1	46	337
9	903849.1.oct	g1958846	67	406	9	903849.1.oct	4897221H1	45	355
9	903849.1.oct	4246274H1	257	505	9	903849.1.oct	2908015H1	41	266
9	903849.1.oct	2814301H1	72	359	9	903849.1.oct	2403093H1	42	249
9	903849.1.oct	485232H1	72	372	9	903849.1.oct	495889H1	43	250
9	903849.1.oct	485973H1	72	315	9	903849.1.oct	3588716H1	42	352

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8	481382.1.oct	2444372H1	129	370
8	481382.1.oct	3344969H1	179	422
8	481382.1.oct	4043328H1	206	389
8	481382.1.oct	2508704H1	252	489
8	481382.1.oct	2370123H1	285	508
8	481382.1.oct	2370123F6	285	610
8	481382.1.oct	2803027H1	308	418
8	481382.1.oct	5335385F6	325	822
8	481382.1.oct	6381567H1	334	534
8	481382.1.oct	1431535H1	378	650
8	481382.1.oct	2755583H1	396	656
8	481382.1.oct	4665103H1	586	848
8	481382.1.oct	2680942H1	1	285
9	903849.1.oct	g3961274	1180	1621
9	903849.1.oct	1380812H1	1191	1421
9	903849.1.oct	g3017243	1195	1610
9	903849.1.oct	2448407T6	1200	1567
9	903849.1.oct	5062263T6	1203	1592
9	903849.1.oct	g1803794	1209	1608
9	903849.1.oct	1697502H1	1209	1417
9	903849.1.oct	g3366973	1210	1614
9	903849.1.oct	g3245013	1219	1611
9	903849.1.oct	g4078415	1223	1614
9	903849.1.oct	g2740706	1225	1614
9	903849.1.oct	g2463862	1227	1612
9	903849.1.oct	g2657445	1228	1610
9	903849.1.oct	1970910H1	1232	1493
9	903849.1.oct	g519042	1234	1610
9	903849.1.oct	g3739697	1238	1614
9	903849.1.oct	g3306909	1240	1614
9	903849.1.oct	g2525781	1243	1438
9	903849.1.oct	g1368047	1253	1599
9	903849.1.oct	g564656	1260	1614
9	903849.1.oct	1696378H1	1261	1440
9	903849.1.oct	2807436F6	1275	1614
9	903849.1.oct	2807436H1	1275	1518
9	903849.1.oct	g1689946	1281	1582
9	903849.1.oct	g1669936	1283	1608
9	903849.1.oct	g2207021	1284	1614
9	903849.1.oct	g751861	1286	1602
9	903849.1.oct	g1140272	1290	1618
9	903849.1.oct	g1136826	1296	1614
9	903849.1.oct	g1801343	1308	1614
9	903849.1.oct	751194H1	1316	1398
9	903849.1.oct	g3179512	1328	1617
9	903849.1.oct	g1231798	1329	1614
9	903849.1.oct	g1124676	1331	1610
9	903849.1.oct	g1648331	1332	1610
9	903849.1.oct	g1241547	1338	1610
9	903849.1.oct	g2945487	1339	1610
9	903849.1.oct	g1693991	1339	1611
9	903849.1.oct	g1229235	1342	1615
9	903849.1.oct	g1018304	1346	1590
9	903849.1.oct	2045971H1	1351	1614
9	903849.1.oct	g1124543	1358	1630
9	903849.1.oct	g1226701	1361	1610
9	903849.1.oct	g2882614	1363	1614
9	903849.1.oct	568980H1	1365	1610
9	903849.1.oct	g890854	1365	1605
9	903849.1.oct	g3644590	1155	1608
9	903849.1.oct	2467148H1	1157	1381
9	903849.1.oct	g3665122	1157	1610
9	903849.1.oct	5099110H1	1161	1424
9	903849.1.oct	g3076029	1366	1617
9	903849.1.oct	g3117308	1366	1614
9	903849.1.oct	g750565	1369	1615
9	903849.1.oct	g518777	1370	1614
9	903849.1.oct	g1368048	1379	1611
9	903849.1.oct	2624665H1	1394	1608
9	903849.1.oct	g2695471	1408	1620
9	903849.1.oct	g2988037	1413	1610
9	903849.1.oct	g2875731	1418	1612
9	903849.1.oct	2120483H1	1423	1602
9	903849.1.oct	899503T1	1431	1572
9	903849.1.oct	899503H1	1431	1610
9	903849.1.oct	2680380H2	1439	1589
9	903849.1.oct	g1331532	1452	1617
9	903849.1.oct	g2806322	1462	1610
9	903849.1.oct	g3093063	1468	1616
9	903849.1.oct	g3041606	1471	1618
9	903849.1.oct	g920645	1481	1617
9	903849.1.oct	2325791H1	1511	1615
9	903849.1.oct	2325782H1	1511	1608
9	903849.1.oct	g4087654	1542	1610
9	903849.1.oct	3165133H1	594	874
9	903849.1.oct	2507856H1	619	878
9	903849.1.oct	g1670047	644	1015
9	903849.1.oct	g890906	646	862
9	903849.1.oct	g751221	653	865
9	903849.1.oct	1255114F6	657	1157
9	903849.1.oct	1255114H1	657	897
9	903849.1.oct	3953586H1	670	893
9	903849.1.oct	2912329H1	676	855
9	903849.1.oct	6181226H1	676	946
9	903849.1.oct	g2459206	684	1109
9	903849.1.oct	2955535H1	696	948
9	903849.1.oct	059142H1	738	937
9	903849.1.oct	1226685H1	746	994
9	903849.1.oct	042939H1	749	1024
9	903849.1.oct	4797142H1	783	1048
9	903849.1.oct	5072193H1	796	1058
9	903849.1.oct	g3166808	838	1077
9	903849.1.oct	4157804H1	845	926
9	903849.1.oct	2252617H1	845	1076
9	903849.1.oct	4716926H1	845	960
9	903849.1.oct	6372420H1	845	1094
9	903849.1.oct	4157804F8	845	1339
9	903849.1.oct	4375829H1	861	1128
9	903849.1.oct	2881017H1	863	1082
9	903849.1.oct	032587H1	871	1016
9	903849.1.oct	2448054F6	871	1320
9	903849.1.oct	g488666	871	1098
9	903849.1.oct	2448062H1	871	1110
9	903849.1.oct	5863686H1	873	1147
9	903849.1.oct	184041H1	876	1090
9	903849.1.oct	4723163H1	878	1074
9	903849.1.oct	4004305H1	907	1163
9	903849.1.oct	3219576H1	930	1275
9	903849.1.oct	3073390H1	937	1208
9	903849.1.oct	466399H1	939	1165
9	903849.1.oct	1929780H1	940	1226
9	903849.1.oct	1929780F6	940	1397
9	903849.1.oct	674013H1	948	1205
9	903849.1.oct	1845763H1	972	1239
9	903849.1.oct	1929780T6	977	1565
9	903849.1.oct	760376R1	986	1465
9	903849.1.oct	760376H1	986	1258
9	903849.1.oct	g1146796	1005	1435
9	903849.1.oct	g1162478	1006	1263
9	903849.1.oct	5598908H1	1013	1286
9	903849.1.oct	3523694H1	1014	1339
9	903849.1.oct	5598808H1	1014	1278
9	903849.1.oct	4466790H1	1017	1280
9	903849.1.oct	2344474T6	1019	1571
9	903849.1.oct	507835H1	1022	1113
9	903849.1.oct	3925430H1	1024	1224

Table 2 cont.

10	433776.4.oct	4618315H1	448	711	11	407607.4.oct	488730H1	129	369
10	433776.4.oct	g3277674	455	863	11	407607.4.oct	488730R1	129	504
10	433776.4.oct	g3596734	458	854	11	407607.4.oct	2697915H1	130	430
10	433776.4.oct	1794582H1	461	741	11	407607.4.oct	492452H1	133	356
10	433776.4.oct	g1521528	465	633	11	407607.4.oct	g758924	146	455
10	433776.4.oct	g1686055	466	848	11	407607.4.oct	3384932H1	154	402
10	433776.4.oct	g1242116	1	486	11	407607.4.oct	2724183H1	168	400
10	433776.4.oct	2968496H1	1	231	11	407607.4.oct	4776138H1	168	424
10	433776.4.oct	6180815H1	3	302	12	234828.6.oct	754031H1	421	672
10	433776.4.oct	3537661H1	8	232	12	234828.6.oct	754031R1	421	865
10	433776.4.oct	1395253H1	11	280	12	234828.6.oct	3872540H1	421	681
10	433776.4.oct	2724859H1	11	269	12	234828.6.oct	1606048H1	423	642
10	433776.4.oct	1616991H1	11	218	12	234828.6.oct	5583855H1	424	664
10	433776.4.oct	1616956H1	11	224	12	234828.6.oct	4931209H1	424	680
10	433776.4.oct	3106763H1	15	306	12	234828.6.oct	2079883H1	424	689
10	433776.4.oct	4921156H1	20	263	12	234828.6.oct	2382770H1	426	561
10	433776.4.oct	1519551H1	20	228	12	234828.6.oct	2765895H1	432	676
10	433776.4.oct	5284327H1	21	266	12	234828.6.oct	474122H1	436	525
10	433776.4.oct	3325136H1	24	296	12	234828.6.oct	6318333H1	457	700
10	433776.4.oct	g2035324	32	235	12	234828.6.oct	2759116H1	470	737
10	433776.4.oct	g1277594	35	625	12	234828.6.oct	g2343422	479	890
10	433776.4.oct	3370603H1	52	339	12	234828.6.oct	2252236H1	494	718
10	433776.4.oct	2819668H1	57	311	12	234828.6.oct	3272534H1	495	682
10	433776.4.oct	1208864H1	75	323	12	234828.6.oct	2874450H1	495	790
10	433776.4.oct	g2037990	123	445	12	234828.6.oct	3467554H1	495	766
10	433776.4.oct	5485307H1	128	406	12	234828.6.oct	6433753H1	519	954
10	433776.4.oct	5485506H1	127	388	12	234828.6.oct	882889H1	527	759
10	433776.4.oct	3570542H1	133	403	12	234828.6.oct	878619H1	527	755
10	433776.4.oct	5426991H1	134	393	12	234828.6.oct	4787945H1	554	810
10	433776.4.oct	5614090H1	166	430	12	234828.6.oct	2470206H1	569	815
10	433776.4.oct	966762H1	173	448	12	234828.6.oct	g1646982	572	925
11	407607.4.oct	g3040496	424	758	12	234828.6.oct	g1629292	572	925
11	407607.4.oct	g3804220	492	758	12	234828.6.oct	1856323H1	583	834
11	407607.4.oct	6383710H1	685	884	12	234828.6.oct	2961901H1	585	875
11	407607.4.oct	2653689H1	695	920	12	234828.6.oct	583034H1	608	847
11	407607.4.oct	2653689F6	695	1081	12	234828.6.oct	4913286H1	623	914
11	407607.4.oct	2704443H1	743	1018	12	234828.6.oct	5579641H1	632	892
11	407607.4.oct	273964H1	821	1112	12	234828.6.oct	147644T6	632	934
11	407607.4.oct	4630477H1	1020	1279	12	234828.6.oct	2018051H1	638	919
11	407607.4.oct	2170060T6	1137	1693	12	234828.6.oct	4696590H1	648	856
11	407607.4.oct	3567607H1	1160	1456	12	234828.6.oct	4089780H1	652	939
11	407607.4.oct	488730F1	1187	1728	12	234828.6.oct	5844923H1	662	896
11	407607.4.oct	g2931185	1236	1731	12	234828.6.oct	479038H1	670	908
11	407607.4.oct	g2804896	1271	1731	12	234828.6.oct	2234295H1	718	883
11	407607.4.oct	678335H1	1299	1562	12	234828.6.oct	4839363H1	735	1003
11	407607.4.oct	g4522930	1324	1730	12	234828.6.oct	1260912T6	860	1148
11	407607.4.oct	g2825971	1344	1728	12	234828.6.oct	1260912H1	909	1124
11	407607.4.oct	g3418650	1350	1729	12	234828.6.oct	g2354133	1049	1528
11	407607.4.oct	534448H1	1473	1715	12	234828.6.oct	1369950R6	1062	1501
11	407607.4.oct	g751634	1475	1731	12	234828.6.oct	1369942H1	1255	1501
11	407607.4.oct	2500372H1	173	414	12	234828.6.oct	1369950H1	1265	1501
11	407607.4.oct	2731329H1	187	360	12	234828.6.oct	2227569H1	31	285
11	407607.4.oct	3664068H1	187	394	12	234828.6.oct	2514489H1	32	330
11	407607.4.oct	5262965H1	213	390	12	234828.6.oct	3574863H1	32	316
11	407607.4.oct	g3118115	368	755	12	234828.6.oct	3421549H1	33	232
11	407607.4.oct	1756214H1	421	650	12	234828.6.oct	2821346H1	35	316
11	407607.4.oct	1336835F6	1530	1728	12	234828.6.oct	2219014H1	37	288
11	407607.4.oct	1336835H1	1530	1728	12	234828.6.oct	2698914H1	37	343
11	407607.4.oct	1336835T6	1533	1683	12	234828.6.oct	3513638H1	38	214
11	407607.4.oct	2598094H1	1612	1736	12	234828.6.oct	1865052H1	37	296
11	407607.4.oct	g3034055	1645	1728	12	234828.6.oct	1865052F6	37	455
11	407607.4.oct	4041804H1	1	286	12	234828.6.oct	g1958966	41	498
11	407607.4.oct	6015486H1	97	359	12	234828.6.oct	1402025H1	39	305
11	407607.4.oct	6098079H1	102	317	12	234828.6.oct	3110477H1	39	344
11	407607.4.oct	4067739H1	110	383	12	234828.6.oct	3127973H1	39	306
11	407607.4.oct	2865508H1	112	393	12	234828.6.oct	551414H1	39	306
11	407607.4.oct	2170060H1	118	382	12	234828.6.oct	3238033H1	39	287
11	407607.4.oct	2170060F6	118	568	12	234828.6.oct	2456375F6	39	431

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9	903849.1.oct	4558109H1	44	183
9	903849.1.oct	2864995H1	44	343
9	903849.1.oct	5641431H1	44	289
9	903849.1.oct	1527073H1	44	245
9	903849.1.oct	5062263F6	46	491
9	903849.1.oct	4172240H1	44	313
9	903849.1.oct	3959981H2	46	322
9	903849.1.oct	4549428H1	45	273
9	903849.1.oct	1527048H1	44	252
9	903849.1.oct	5062295H1	46	292
9	903849.1.oct	256106H1	47	217
9	903849.1.oct	g1648330	47	208
9	903849.1.oct	g1638232	46	361
9	903849.1.oct	g519043	53	390
9	903849.1.oct	4550411H1	59	145
9	903849.1.oct	4777779H1	57	341
9	903849.1.oct	3222580H1	57	358
10	433776.4.oct	5033631H1	469	737
10	433776.4.oct	g1687856	472	854
10	433776.4.oct	2293262H1	471	711
10	433776.4.oct	1354926H1	471	707
10	433776.4.oct	4465127H1	471	715
10	433776.4.oct	1354926F1	471	854
10	433776.4.oct	6380506H1	474	773
10	433776.4.oct	390032H1	474	742
10	433776.4.oct	1396456H1	474	736
10	433776.4.oct	g617480	496	864
10	433776.4.oct	893675H1	496	796
10	433776.4.oct	1289927H1	496	628
10	433776.4.oct	893675T2	496	821
10	433776.4.oct	g1227083	498	854
10	433776.4.oct	g4266355	507	796
10	433776.4.oct	g2557641	508	796
10	433776.4.oct	g2268469	510	796
10	433776.4.oct	g3755408	510	796
10	433776.4.oct	g2047133	517	796
10	433776.4.oct	g3400966	517	796
10	433776.4.oct	3929730H1	519	794
10	433776.4.oct	763300H1	537	767
10	433776.4.oct	g3087068	540	796
10	433776.4.oct	g2437132	547	875
10	433776.4.oct	g615017	549	846
10	433776.4.oct	g4332629	553	796
10	433776.4.oct	g618161	553	796
10	433776.4.oct	g3785364	558	796
10	433776.4.oct	g2958569	573	796
10	433776.4.oct	g3960831	574	796
10	433776.4.oct	g2821439	583	796
10	433776.4.oct	755596R1	591	796
10	433776.4.oct	755596H1	591	796
10	433776.4.oct	g820638	597	875
10	433776.4.oct	1572358H1	597	768
10	433776.4.oct	g561098	604	796
10	433776.4.oct	4713167H1	612	796
10	433776.4.oct	2046173H1	616	812
10	433776.4.oct	1343446H1	618	796
10	433776.4.oct	g1521690	629	796
10	433776.4.oct	2008986H1	629	811
10	433776.4.oct	1616956T6	635	796
10	433776.4.oct	g4333263	641	796
10	433776.4.oct	4173546H1	646	797
10	433776.4.oct	g4270379	647	863
10	433776.4.oct	g4450858	652	796
10	433776.4.oct	2229690H1	656	858
10	433776.4. ct	6387415H1	661	942
10	433776.4.oct	g3430941	677	796
10	433776.4.oct	2352669H1	680	796
10	433776.4.oct	g3052821	719	796
10	433776.4.oct	1726524H1	722	854
10	433776.4.oct	1724358H1	722	796
10	433776.4.oct	2459364H1	743	796
10	433776.4.oct	g3841157	744	796
10	433776.4.oct	5451747H1	173	428
10	433776.4.oct	3603250H1	183	485
10	433776.4.oct	3571124H1	185	494
10	433776.4.oct	6014182H1	192	422
10	433776.4.oct	1004309R1	192	661
10	433776.4.oct	1923125H1	194	459
10	433776.4.oct	3969881H1	194	464
10	433776.4.oct	1004309H1	192	456
10	433776.4.oct	g1678417	195	511
10	433776.4.oct	1504030H1	199	456
10	433776.4.oct	g1940320	201	567
10	433776.4.oct	g2556305	210	433
10	433776.4.oct	g2554138	212	626
10	433776.4.oct	4763891H1	226	483
10	433776.4.oct	4266849H1	228	348
10	433776.4.oct	4350779H1	231	332
10	433776.4.oct	1724295T6	277	798
10	433776.4.oct	567093H1	269	425
10	433776.4.oct	608247H1	270	529
10	433776.4.oct	607814H1	270	545
10	433776.4.oct	6093674H1	272	570
10	433776.4.oct	939181H1	293	592
10	433776.4.oct	1006147H1	300	577
10	433776.4.oct	5427972H1	300	558
10	433776.4.oct	1923769H1	320	573
10	433776.4.oct	1923769R6	322	727
10	433776.4.oct	2411986H1	322	552
10	433776.4.oct	4511411H1	322	579
10	433776.4.oct	2540387H1	331	563
10	433776.4.oct	6078678H1	331	531
10	433776.4.oct	934752H1	335	575
10	433776.4.oct	934752R1	335	807
10	433776.4.oct	2010868H1	334	532
10	433776.4.oct	934752T1	335	816
10	433776.4.oct	5273207H1	347	601
10	433776.4.oct	4160027H1	349	611
10	433776.4.oct	2430254H1	355	605
10	433776.4.oct	4850377H1	363	636
10	433776.4.oct	g1847829	369	805
10	433776.4.oct	1223654H1	381	507
10	433776.4.oct	1223654T1	380	810
10	433776.4.oct	g1987932	380	646
10	433776.4.oct	5275279H1	387	561
10	433776.4.oct	1867144H1	387	625
10	433776.4.oct	g2276753	399	753
10	433776.4.oct	g4153602	402	853
10	433776.4.oct	g3756942	403	857
10	433776.4.oct	g3596025	405	854
10	433776.4.oct	807740H1	406	592
10	433776.4.oct	808336H1	406	575
10	433776.4.oct	4820231H1	406	595
10	433776.4.oct	3238233H1	413	666
10	433776.4.oct	1616991T6	416	816
10	433776.4.oct	g3734566	416	857
10	433776.4.oct	g4088877	419	857
10	433776.4.oct	g4069104	420	854
10	433776.4.oct	1493172H1	431	669
10	433776.4. ct	2005329H1	431	619
10	433776.4.oct	g1847522	437	852
10	433776.4.oct	g3425153	441	869
10	433776.4.oct	g1210346	443	856
10	433776.4.oct	g3679055	446	849
10	433776.4.oct	4619401H1	448	733
10	433776.4.oct	4619137H1	449	704

Table 2 cont.

13	336430.2.dec	g2568596	946	1420	14	242269.2.dec	g3446472	8	341
13	336430.2.d c	5327737H1	952	1199	14	242269.2.dec	g1300544	6	304
13	336430.2.dec	5328936H1	952	1185	14	242269.2.dec	g1300552	6	191
13	336430.2.dec	g3872395	958	1421	14	242269.2.dec	g3092388	8	186
13	336430.2.dec	g5365162	963	1421	14	242269.2.dec	g4664448	8	459
13	336430.2.dec	g3649273	963	1421	14	242269.2.dec	g5176993	9	472
13	336430.2.dec	g3807210	966	1422	14	242269.2.dec	g4080641	9	410
13	336430.2.dec	g5110447	967	1425	14	242269.2.dec	g3755968	8	392
13	336430.2.dec	g2094368	980	1433	14	242269.2.dec	g4987817	8	359
13	336430.2.dec	g2094705	982	1433	14	242269.2.dec	g4195319	8	208
13	336430.2.dec	g3756305	999	1424	14	242269.2.dec	1351344F1	12	378
13	336430.2.dec	g3306777	1007	1421	14	242269.2.dec	410843H1	12	61
13	336430.2.dec	1696181H1	1015	1229	14	242269.2.dec	410843R1	12	501
13	336430.2.dec	g4088599	1030	1421	14	242269.2.dec	418126H1	12	218
13	336430.2.dec	g2789183	1032	1430	14	242269.2.dec	414883H1	12	185
13	336430.2.dec	g3597567	1032	1436	14	242269.2.dec	1560349F6	12	184
13	336430.2.dec	g2905080	1036	1421	14	242269.2.dec	414473H1	12	171
13	336430.2.dec	g2210720	1043	1430	14	242269.2.dec	415911H1	12	171
13	336430.2.dec	g2656576	1045	1422	14	242269.2.dec	412381H1	12	164
13	336430.2.dec	g4081784	1065	1427	14	242269.2.dec	855180H1	12	145
13	336430.2.dec	g1398311	1065	1403	14	242269.2.dec	g5101470	12	410
13	336430.2.dec	g2555670	1085	1423	14	242269.2.dec	g1859732	12	297
13	336430.2.dec	g5673404	1086	1425	14	242269.2.dec	g817501	67	430
13	336430.2.dec	g3086789	1087	1426	14	242269.2.dec	g5232210	72	521
13	336430.2.dec	g3843266	1100	1422	14	242269.2.dec	g2569754	74	507
13	336430.2.dec	g4598223	1105	1431	14	242269.2.dec	g4074654	75	485
13	336430.2.dec	g1391454	1107	1422	14	242269.2.dec	g5444203	75	389
13	336430.2.dec	g752027	1127	1424	14	242269.2.dec	6268308H1	75	348
13	336430.2.dec	g2905252	1136	1421	14	242269.2.dec	g1202202	75	239
13	336430.2.dec	g2111314	1159	1423	14	242269.2.dec	118555T6	84	585
13	336430.2.dec	g2818409	1165	1421	14	242269.2.dec	6614443H1	84	583
13	336430.2.dec	g1266907	1166	1421	14	242269.2.dec	1222034H1	88	258
13	336430.2.dec	g3172766	1206	1422	14	242269.2.dec	1222034T1	88	258
13	336430.2.dec	g2809576	1212	1421	14	242269.2.dec	4032139H1	88	213
13	336430.2.dec	g3872913	1227	1427	14	242269.2.dec	1560349T6	88	191
13	336430.2.dec	g2807042	1233	1425	14	242269.2.dec	942024T1	88	184
13	336430.2.dec	g3431342	1242	1421	14	242269.2.dec	g4690294	88	350
13	336430.2.dec	g3431049	1267	1421	14	242269.2.dec	1972779H1	105	338
13	336430.2.dec	g3233026	1272	1421	14	242269.2.dec	1351344H1	126	378
13	336430.2.dec	g2138890	1273	1411	14	242269.2.dec	1565904H1	128	349
13	336430.2.dec	g1887337	1285	1421	14	242269.2.dec	5812349H1	146	472
13	336430.2.dec	g3092413	1291	1425	14	242269.2.dec	5328191H1	156	395
13	336430.2.dec	1559410T6	1301	1379	14	242269.2.dec	3515332H1	160	417
14	242269.2.dec	g1242484	1	297	14	242269.2.dec	3787803H1	173	279
14	242269.2.dec	g5236089	1	458	14	242269.2.dec	5531343H1	229	471
14	242269.2.dec	g3017107	1	274	14	242269.2.dec	5979339H1	234	533
14	242269.2.dec	g2716604	1	77	14	242269.2.dec	4407739H1	240	303
14	242269.2.dec	g3539600	1	355	14	242269.2.dec	754264H1	310	524
14	242269.2.dec	g5528437	1	281	14	242269.2.dec	1756754R6	344	612
14	242269.2.dec	1560349H1	2	184	14	242269.2.dec	410843F1	365	952
14	242269.2.dec	g1281302	2	415	14	242269.2.dec	4312365H1	366	672
14	242269.2.dec	g3182199	3	245	14	242269.2.dec	5391660H1	390	660
14	242269.2.dec	g4070944	3	408	14	242269.2.dec	1671523H1	392	587
14	242269.2.dec	g5235258	5	465	14	242269.2.dec	2911066H1	396	676
14	242269.2.dec	g5232045	5	346	14	242269.2.dec	5392390H1	394	661
14	242269.2.dec	g3679020	5	382	14	242269.2.dec	5913540H1	420	699
14	242269.2.dec	1351344F6	8	378	14	242269.2.dec	1456573H1	430	708
14	242269.2.dec	g5101469	7	411	14	242269.2.dec	1427238H1	443	689
14	242269.2.dec	g2167296	5	353	14	242269.2.dec	2398593H1	450	675
14	242269.2.dec	g5232575	8	457	14	242269.2.dec	6265863H1	454	1030
14	242269.2.dec	942024H1	8	184	14	242269.2.dec	g1317243	476	894
14	242269.2.dec	942024R1	8	184	14	242269.2.dec	g1317236	505	895
14	242269.2.dec	3127564H1	8	141	14	242269.2.dec	g1975087	512	773
14	242269.2.dec	g4436066	8	454	14	242269.2.dec	5508442H1	582	830
14	242269.2.dec	g4850437	8	398	14	242269.2.dec	1525743H1	665	810
14	242269.2.dec	g2740407	8	391	14	242269.2.dec	5193340H1	764	874
14	242269.2.dec	g3231712	8	362	14	242269.2.dec	4669147H1	768	1016
14	242269.2.dec	g3427933	8	350	14	242269.2.dec	411214H1	1	241

Table 2 cont.

12	234828.6.oct	3461179H1	39	300
12	234828.6.oct	990620H1	37	332
12	234828.6.oct	2857770H1	39	295
12	234828.6.oct	2456375H1	39	279
12	234828.6.oct	1452171H1	40	294
12	234828.6.oct	2443307H1	40	280
12	234828.6.oct	2477496H1	40	270
12	234828.6.oct	729737H1	41	270
12	234828.6.oct	729737R1	41	381
12	234828.6.oct	3482624H1	41	193
12	234828.6.oct	3199337H1	45	309
12	234828.6.oct	1340368H1	45	222
12	234828.6.oct	4265872H1	45	242
12	234828.6.oct	3871172H1	46	318
12	234828.6.oct	2202960H1	46	284
12	234828.6.oct	1839888H1	46	286
12	234828.6.oct	1823204H1	46	263
12	234828.6.oct	2740138H1	53	295
12	234828.6.oct	5488475H1	71	321
12	234828.6.oct	5119401H1	101	377
12	234828.6.oct	6158348H1	139	414
12	234828.6.oct	g1967590	153	615
12	234828.6.oct	2345622H1	155	403
12	234828.6.oct	2241354H1	171	421
12	234828.6.oct	3687713H1	171	478
12	234828.6.oct	5895482H1	172	431
12	234828.6.oct	5469071H1	174	421
12	234828.6.oct	5468888H1	174	440
12	234828.6.oct	1453408H1	177	391
12	234828.6.oct	096223H1	213	459
12	234828.6.oct	508399H1	225	443
12	234828.6.oct	2473672H1	240	462
12	234828.6.oct	3858095H1	240	465
12	234828.6.oct	2300564H1	242	513
12	234828.6.oct	4650680H1	244	528
12	234828.6.oct	1753653H1	253	471
12	234828.6.oct	1751064H1	253	455
12	234828.6.oct	1613647H1	260	421
12	234828.6.oct	1400857H1	280	536
12	234828.6.oct	1338695H1	295	575
12	234828.6.oct	887176H1	294	436
12	234828.6.oct	2109128H1	296	560
12	234828.6.oct	2668260H1	321	563
12	234828.6.oct	755666H1	333	591
12	234828.6.oct	711736H1	351	588
12	234828.6.oct	3622670H1	353	601
12	234828.6.oct	616778H1	359	589
12	234828.6.oct	4399919H1	361	514
12	234828.6.oct	4399967H1	361	463
12	234828.6.oct	3622723H1	371	653
12	234828.6.oct	5881854H1	371	604
12	234828.6.oct	5888129H1	373	628
12	234828.6.oct	5885158H1	373	538
12	234828.6.oct	3407432F6	406	831
12	234828.6.oct	1998763H1	406	615
12	234828.6.oct	2456375T6	406	916
12	234828.6.oct	3407432H1	408	520
12	234828.6.oct	3696963H1	407	684
12	234828.6.oct	3282868H1	1	261
12	234828.6.oct	3538688H1	13	279
12	234828.6.oct	2440643H1	14	266
12	234828.6.oct	1502680H1	14	302
12	234828.6.oct	2972804H2	15	316
12	234828.6.oct	1508218H1	20	194
12	234828.6.oct	3230962H1	25	314
12	234828.6.oct	1492324H1	25	245
12	234828.6.oct	3148621H1	25	294
12	234828.6.oct	618656H1	25	295
12	234828.6.oct	2670605H1	25	307
12	234828.6.oct	3385262H1	27	295
12	234828.6.oct	1334746H1	27	277
12	234828.6.oct	3370289H1	26	130
12	234828.6.oct	6176386H1	27	316
12	234828.6.oct	1502616H1	14	256
12	234828.6.oct	3591749H1	27	329
12	234828.6.oct	2443723H1	27	253
12	234828.6.oct	3204501H1	28	153
12	234828.6.oct	2015825H1	28	327
12	234828.6.oct	2733437H1	28	269
12	234828.6.oct	2198080H1	29	287
12	234828.6.oct	1444948H1	29	296
12	234828.6.oct	2961687H1	29	303
12	234828.6.oct	6179991H1	29	289
12	234828.6.oct	2198495H1	29	191
12	234828.6.oct	2906122H1	29	128
12	234828.6.oct	3297819H1	29	263
12	234828.6.oct	2901213H1	30	121
12	234828.6.oct	2782627H1	29	279
12	234828.6.oct	1625443H1	29	268
12	234828.6.oct	6178209H1	30	303
12	234828.6.oct	3208193H1	29	297
13	336430.2.dec	3593730H1	1	168
13	336430.2.dec	2781490H1	1	242
13	336430.2.dec	3882669H1	7	296
13	336430.2.dec	3520838H1	19	347
13	336430.2.dec	3574135H1	19	146
13	336430.2.dec	1559410H1	29	247
13	336430.2.dec	1559410F6	29	229
13	336430.2.dec	2266238H1	29	181
13	336430.2.dec	1299583H1	31	227
13	336430.2.dec	3045047H1	34	164
13	336430.2.dec	1227115H1	35	277
13	336430.2.dec	1535201H1	45	257
13	336430.2.dec	g1300630	105	520
13	336430.2.dec	g2111158	157	360
13	336430.2.dec	2387085H1	240	425
13	336430.2.dec	g2210797	269	725
13	336430.2.dec	3761768H1	281	583
13	336430.2.dec	6544503H1	305	802
13	336430.2.dec	4062190H1	344	512
13	336430.2.dec	6362028H1	396	898
13	336430.2.dec	g2409916	413	726
13	336430.2.dec	5041464H1	423	681
13	336430.2.dec	5271874H1	452	533
13	336430.2.dec	4637615H1	486	726
13	336430.2.dec	4000922H1	511	678
13	336430.2.dec	1811269F6	603	1033
13	336430.2.dec	1811269H1	603	860
13	336430.2.dec	5106212H1	659	921
13	336430.2.dec	g2094638	671	1091
13	336430.2.dec	g2094369	676	1077
13	336430.2.dec	1688367F6	681	1229
13	336430.2.dec	1688376H1	681	916
13	336430.2.dec	1688985H1	681	895
13	336430.2.dec	4003277H1	714	978
13	336430.2.dec	g1891651	735	1123
13	336430.2.dec	5604707H1	738	1013
13	336430.2.dec	536938H1	741	976
13	336430.2.dec	537096H1	741	898
13	336430.2.dec	6123126H1	751	1347
13	336430.2.dec	1809306H1	757	1009
13	336430.2.dec	6309359H1	786	1379
13	336430.2.dec	2275833H1	797	1015
13	336430.2.d c	3805902H1	830	1108
13	336430.2.dec	1811269T6	830	1379
13	336430.2.dec	3998808H1	934	1230

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18	235983.6.dec	g390184	2995	3311	18	235983.6.dec	2465140H1	3782	4006
18	235983.6.d c	4220392H1	3005	3279	18	235983.6.dec	g3174357	3788	4082
18	235983.6.dec	3286977H1	3012	3260	18	235983.6.d c	4024334H1	3790	4081
18	235983.6.dec	g616559	3020	3327	18	235983.6.dec	1499362H1	3787	3978
18	235983.6.dec	2192319H1	3033	3264	18	235983.6.dec	4646510H1	3789	4056
18	235983.6.dec	5683292H1	3051	3287	18	235983.6.d c	1594535H1	3789	3999
18	235983.6.dec	4182518H1	3054	3332	18	235983.6.dec	898100H1	3797	4054
18	235983.6.dec	926283H1	3062	3334	18	235983.6.dec	4837242H1	3798	4012
18	235983.6.dec	3491246H1	3067	3343	18	235983.6.dec	898100R1	3797	4374
18	235983.6.dec	4601526H1	3068	3332	18	235983.6.dec	4837492H1	3799	4086
18	235983.6.dec	g883924	3070	3132	18	235983.6.dec	3573408H1	3799	4096
18	235983.6.dec	4898255H1	3078	3326	18	235983.6.dec	4837274H1	3799	4053
18	235983.6.dec	g612635	3095	3379	18	235983.6.dec	g1391806	3807	4225
18	235983.6.dec	1501609H1	3091	3287	18	235983.6.dec	g4901871	3806	4225
18	235983.6.dec	5435484H1	3095	3275	18	235983.6.dec	5861440H1	3806	4093
18	235983.6.dec	1710332H1	3109	3332	18	235983.6.dec	5152105H1	3809	4084
18	235983.6.dec	3706933H1	3120	3405	18	235983.6.dec	833965H1	3809	4080
18	235983.6.dec	991301H1	3125	3430	18	235983.6.dec	g2331330	3810	4124
18	235983.6.dec	991301R1	3125	3561	18	235983.6.dec	2053601H1	3815	4070
18	235983.6.dec	4670213H1	3130	3378	18	235983.6.dec	903670H1	3815	4007
18	235983.6.dec	1815401T6	3640	4185	18	235983.6.dec	2875944H1	3816	4091
18	235983.6.dec	5610495H1	3639	3898	18	235983.6.dec	4402735H1	3816	4074
18	235983.6.dec	g1050006	3647	3981	18	235983.6.dec	5530194H1	3820	4068
18	235983.6.dec	g711179	3646	3848	18	235983.6.dec	g2752396	3818	4234
18	235983.6.dec	1317687H1	3646	3820	18	235983.6.dec	6009383H1	3826	4108
18	235983.6.dec	1968426H1	3656	3917	18	235983.6.dec	g2873872	3825	4228
18	235983.6.dec	878460R1	3658	4226	18	235983.6.dec	3658872H1	3833	4112
18	235983.6.dec	4933278H1	3657	3929	18	235983.6.dec	g1153144	3831	4237
18	235983.6.dec	4110987H1	3658	3755	18	235983.6.dec	2500844H1	3842	4072
18	235983.6.dec	878460H1	3658	3909	18	235983.6.dec	6312876H1	3844	4372
18	235983.6.dec	2195022H1	3661	3903	18	235983.6.dec	1428214T6	3849	4185
18	235983.6.dec	4152080H1	3664	3925	18	235983.6.dec	2244834H1	3850	4105
18	235983.6.dec	984860R1	3667	4117	18	235983.6.dec	g3869186	1	4539
18	235983.6.dec	984860H1	3667	3888	18	235983.6.dec	3699775H1	61	346
18	235983.6.dec	3573936H1	3673	3955	18	235983.6.dec	5047477H1	147	377
18	235983.6.dec	3088228H1	3677	3952	18	235983.6.dec	3381586H1	145	394
18	235983.6.dec	1781737H1	3680	3878	18	235983.6.dec	6484838H1	146	679
18	235983.6.dec	g2053250	3686	4062	18	235983.6.dec	3584956H1	147	464
18	235983.6.dec	4254583H1	3687	3941	18	235983.6.dec	6476413H1	148	678
18	235983.6.dec	g1101456	3688	3907	18	235983.6.dec	5047477F6	147	671
18	235983.6.dec	g982339	3689	4031	18	235983.6.dec	6476530H1	148	663
18	235983.6.dec	g1042775	3689	3974	18	235983.6.dec	5047423H1	147	346
18	235983.6.dec	6350466H2	3692	4013	18	235983.6.dec	3586619H1	147	341
18	235983.6.dec	3624071H1	3692	3876	18	235983.6.dec	3073571H1	147	432
18	235983.6.dec	4425320H1	3694	3970	18	235983.6.dec	353081H1	154	378
18	235983.6.dec	4793731H1	3698	3978	18	235983.6.dec	3288503H1	155	418
18	235983.6.dec	4991525H1	3699	3981	18	235983.6.dec	121178H1	160	232
18	235983.6.dec	2346595H1	3699	3952	18	235983.6.dec	g2703916	489	726
18	235983.6.dec	2666581H1	3699	3942	18	235983.6.dec	3119591H1	505	773
18	235983.6.dec	3203383H1	3702	3961	18	235983.6.dec	g4104518	611	2596
18	235983.6.dec	g1046477	3719	4063	18	235983.6.dec	g1471244	675	725
18	235983.6.dec	g714049	3719	4027	18	235983.6.dec	4994487H1	916	1180
18	235983.6.dec	5471836H1	3725	3984	18	235983.6.dec	3353480H2	953	1127
18	235983.6.dec	3692694H1	3739	4020	18	235983.6.dec	1477782H1	1030	1238
18	235983.6.dec	3345345H1	3741	3983	18	235983.6.dec	5950615H1	1047	1298
18	235983.6.dec	2530908H1	3749	3999	18	235983.6.dec	2525583F7	1097	1544
18	235983.6.dec	1446674H1	3760	4024	18	235983.6.dec	2525583H1	1097	1343
18	235983.6.dec	1397742H1	3761	4023	18	235983.6.dec	434615H1	1122	1347
18	235983.6.dec	1400409H1	3761	3975	18	235983.6.dec	5153342H1	1281	1547
18	235983.6.dec	g1141309	3767	4119	18	235983.6.dec	6281520H1	1337	1611
18	235983.6.dec	3916312H1	3768	4052	18	235983.6.dec	531966H1	1353	1596
18	235983.6.dec	4598159H1	3771	4029	18	235983.6.dec	2608473F6	1364	1818
18	235983.6.dec	855084H1	3777	4024	18	235983.6.d c	2608473H1	1364	1582
18	235983.6.dec	855084R1	3777	4168	18	235983.6.dec	6282763H1	1367	1611
18	235983.6.dec	382681H1	3777	3922	18	235983.6.dec	6289464H1	1407	1611
18	235983.6.dec	4511379H1	3779	4009	18	235983.6.d c	4997470H1	1419	1674
18	235983.6.dec	g2806189	3780	4225	18	235983.6.dec	6006170H1	1421	1697
18	235983.6.dec	1964217H1	3782	4051	18	235983.6.dec	6285201H1	1430	1611

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15	432120.2.d c	6245865H1	1	593
15	432120.2.dec	6244465H1	1	511
15	432120.2.dec	g4078434	161	593
15	432120.2.dec	g3765386	212	592
16	198060.6.dec	2124623H1	1	293
16	198060.6.dec	1669868F6	1	485
16	198060.6.dec	1668592H1	1	237
16	198060.6.dec	1669868H1	1	225
16	198060.6.dec	g2163372	12	479
16	198060.6.dec	4217360H1	15	235
16	198060.6.dec	3115007H1	19	295
16	198060.6.dec	3296971H1	19	278
16	198060.6.dec	582217H1	22	284
16	198060.6.dec	6314762H1	22	542
16	198060.6.dec	2074567H1	22	269
16	198060.6.dec	2502240H1	22	260
16	198060.6.dec	1646819H1	24	225
16	198060.6.dec	754097R1	31	540
16	198060.6.dec	754097H1	31	230
16	198060.6.dec	1216727H1	26	268
16	198060.6.dec	1626708H1	26	242
16	198060.6.dec	g846944	28	340
16	198060.6.dec	g1897607	29	463
16	198060.6.dec	3669190H1	29	332
16	198060.6.dec	3254637H1	30	272
16	198060.6.dec	2769479H1	31	270
16	198060.6.dec	3521542H1	35	304
16	198060.6.dec	g2154340	34	494
16	198060.6.dec	g2055182	34	424
16	198060.6.dec	5899676H1	34	290
16	198060.6.dec	4116735H1	35	303
16	198060.6.dec	2078062H1	34	324
16	198060.6.dec	g2240557	39	394
16	198060.6.dec	6168723H1	52	377
16	198060.6.dec	4155225H1	75	338
16	198060.6.dec	1395663H1	76	321
16	198060.6.dec	5947207H1	80	386
16	198060.6.dec	1615709F6	86	409
16	198060.6.dec	1615709H1	86	303
16	198060.6.dec	1615658H1	86	291
16	198060.6.dec	6121415H1	86	552
16	198060.6.dec	4976055H1	109	384
16	198060.6.dec	5571129H1	136	338
16	198060.6.dec	591629H1	148	407
16	198060.6.dec	g2505783	153	550
16	198060.6.dec	3842850H1	155	466
16	198060.6.dec	2876041H1	163	435
16	198060.6.dec	4643178H1	167	432
16	198060.6.dec	g2251559	185	494
16	198060.6.dec	4307771H1	214	557
16	198060.6.dec	1971942F6	230	599
16	198060.6.dec	1971942H1	230	462
16	198060.6.dec	4139057H1	244	528
16	198060.6.dec	1886793F6	248	613
16	198060.6.dec	1886793H1	248	502
16	198060.6.dec	1736029H1	265	479
16	198060.6.dec	1527256H1	260	471
16	198060.6.dec	1527264H1	260	474
16	198060.6.dec	5884461H1	285	490
16	198060.6.dec	g5639170	373	551
16	198060.6.dec	4913811H1	437	555
16	198060.6.dec	4409109H1	419	701
16	198060.6.dec	4611874H1	489	554
16	198060.6.d c	232531H1	514	670
16	198060.6.d c	2829981H1	516	786
16	198060.6.d c	4795943H1	662	919
16	198060.6.d c	3340413H1	669	917
17	460295.5.d c	6314460H1	1	520
17	460295.5.dec	g3367188	56	521
17	460295.5.dec	g4080100	56	454
17	460295.5.dec	g4729190	56	373
17	460295.5.dec	g4088006	56	237
17	460295.5.dec	g2342207	58	484
17	460295.5.dec	g3989464	74	509
17	460295.5.dec	319592H1	118	493
17	460295.5.dec	g2955006	144	520
17	460295.5.dec	g3173296	144	430
18	235983.6.dec	4299850H1	440	643
18	235983.6.dec	4029867H1	2089	2328
18	235983.6.dec	3237027H1	2138	2384
18	235983.6.dec	3698637H1	2157	2417
18	235983.6.dec	1389014H1	2170	2418
18	235983.6.dec	3576941H1	2186	2450
18	235983.6.dec	1428214F6	2184	2659
18	235983.6.dec	1428214H1	2184	2422
18	235983.6.dec	352928H1	2204	2420
18	235983.6.dec	1477331H1	2225	2479
18	235983.6.dec	5065937H1	2227	2422
18	235983.6.dec	5545038H1	2233	2409
18	235983.6.dec	370706H1	2249	2461
18	235983.6.dec	4342101H1	2253	2564
18	235983.6.dec	3115093H1	2282	2540
18	235983.6.dec	1675942F6	2323	2744
18	235983.6.dec	1675942H1	2323	2570
18	235983.6.dec	g1727349	2329	2644
18	235983.6.dec	2224812H1	2355	2597
18	235983.6.dec	4171462H1	2414	2677
18	235983.6.dec	g1939837	2426	2907
18	235983.6.dec	183492H1	2478	2651
18	235983.6.dec	g1812050	2489	2872
18	235983.6.dec	3959415H1	2505	2644
18	235983.6.dec	g2002932	2512	2877
18	235983.6.dec	g4152315	2525	2928
18	235983.6.dec	2115214H1	2522	2802
18	235983.6.dec	g1391919	2545	2914
18	235983.6.dec	g1492984	2545	2757
18	235983.6.dec	5616747H1	2676	2965
18	235983.6.dec	6097857H1	2686	2978
18	235983.6.dec	971194H1	2701	2963
18	235983.6.dec	2695292H1	2747	3032
18	235983.6.dec	4434429H1	2763	3040
18	235983.6.dec	g2002465	2773	3189
18	235983.6.dec	g390429	2778	3084
18	235983.6.dec	3875830H1	2776	3038
18	235983.6.dec	4935114H1	2782	2880
18	235983.6.dec	g772632	2784	3120
18	235983.6.dec	4828524H1	2804	3005
18	235983.6.dec	1502463H1	2811	3087
18	235983.6.dec	1502565H1	2811	3078
18	235983.6.dec	g4152317	2817	3146
18	235983.6.dec	2319441H1	2852	3099
18	235983.6.dec	188577H1	2864	3008
18	235983.6.dec	476050H1	2887	3150
18	235983.6.dec	g2053717	2895	3218
18	235983.6.dec	1642393H1	2901	3100
18	235983.6.dec	4760790H1	2907	3195
18	235983.6.dec	4721402H1	2907	3186
18	235983.6.dec	4721224H1	2907	3165
18	235983.6.dec	2667314H1	2954	3199
18	235983.6.dec	1815401F6	2956	3354
18	235983.6.d c	1815401H1	2956	3214
18	235983.6.dec	1393159H1	2956	3209
18	235983.6.dec	1393191H1	2956	3210
18	235983.6.dec	2155279H1	2958	3206
18	235983.6.dec	3870754H1	2966	3258
18	235983.6.dec	3855427H1	2979	3261

Table 2 cont.

18	235983.6.dec	4301987H1	4164	4405	18	235983.6.dec	g718586	4278	4517
18	235983.6.dec	g1773776	4165	4409	18	235983.6.dec	g2445128	4285	4534
18	235983.6.dec	3419076T6	4197	4508	18	235983.6.dec	g2053618	4285	4537
18	235983.6.dec	g1264115	4202	4539	18	235983.6.dec	2563295H1	4289	4541
18	235983.6.dec	928449T6	4210	4501	18	235983.6.dec	g1049755	4299	4546
18	235983.6.d c	g4874751	4210	4545	18	235983.6.dec	g779371	4300	4545
18	235983.6.dec	2005565H1	4213	4413	18	235983.6.dec	1979178H1	4299	4539
18	235983.6.dec	g1148504	4215	4539	18	235983.6.dec	g3871331	4305	4539
18	235983.6.dec	g866362	4219	4545	18	235983.6.dec	910538H1	4312	4533
18	235983.6.dec	3956647H1	4219	4508	18	235983.6.dec	549362F1	4335	4541
18	235983.6.dec	4359163H1	4220	4447	18	235983.6.dec	2275266H1	4338	4539
18	235983.6.dec	g883309	4224	4567	18	235983.6.dec	549362H1	4346	4541
18	235983.6.dec	g723173	4223	4525	18	235983.6.dec	3808941H1	4346	4533
18	235983.6.dec	g3840912	4225	4544	18	235983.6.dec	g2589294	4349	4547
18	235983.6.dec	g2986196	4228	4541	18	235983.6.dec	287095H1	4351	4533
18	235983.6.dec	g2715739	4227	4536	18	235983.6.dec	2662364F6	4364	4533
18	235983.6.dec	g1046478	4227	4507	18	235983.6.dec	2662364H1	4364	4533
18	235983.6.dec	g4088760	4230	4533	18	235983.6.dec	5847389H1	4366	4533
18	235983.6.dec	g3425690	4230	4533	18	235983.6.dec	5872270H1	4369	4441
18	235983.6.dec	4466803H1	4231	4383	18	235983.6.dec	4298534H1	4372	4539
18	235983.6.dec	767529H1	4236	4471	18	235983.6.dec	g1210948	4383	4542
18	235983.6.dec	g612988	4237	4541	18	235983.6.dec	g1137312	4397	4541
18	235983.6.dec	g2817035	4237	4539	18	235983.6.dec	811100T1	4419	4497
18	235983.6.dec	2430718H1	4239	4477	18	235983.6.dec	811100H1	4419	4527
18	235983.6.dec	g5510981	4243	4554	18	235983.6.dec	g2270136	4429	4534
18	235983.6.dec	g3279191	4243	4545	18	235983.6.dec	233542H1	4430	4533
18	235983.6.dec	3040021H1	4243	4450	18	235983.6.dec	g982292	4450	4512
18	235983.6.dec	219012H1	4243	4405	18	235983.6.dec	g1792123	4452	4539
18	235983.6.dec	5566988H1	4243	4376	18	235983.6.dec	g3057972	4466	4542
18	235983.6.dec	g1860203	4243	4544	18	235983.6.dec	g3839889	4479	4548
18	235983.6.dec	g3769996	4243	4543	18	235983.6.dec	4467167H1	4479	4533
18	235983.6.dec	g3057160	4243	4543	18	235983.6.dec	g1691482	4487	4543
18	235983.6.dec	g2206143	4243	4547	18	235983.6.dec	2942208H2	3134	3398
18	235983.6.dec	g3231269	4243	4546	18	235983.6.dec	3500378H1	3137	3430
18	235983.6.dec	g3933929	4243	4541	18	235983.6.dec	3873691H1	3143	3409
18	235983.6.dec	g4152314	4243	4541	18	235983.6.dec	4644974H1	3144	3402
18	235983.6.dec	g3917367	4243	4539	18	235983.6.dec	3620275H1	3158	3412
18	235983.6.dec	g3331035	4243	4539	18	235983.6.dec	5198954H1	3158	3327
18	235983.6.dec	g2741042	4243	4540	18	235983.6.dec	6412923H1	3158	3514
18	235983.6.dec	g5541034	4243	4538	18	235983.6.dec	4692566H1	3168	3408
18	235983.6.dec	g3675471	4243	4538	18	235983.6.dec	4941568H1	3169	3437
18	235983.6.dec	g3091778	4243	4533	18	235983.6.dec	3680473H1	3185	3467
18	235983.6.dec	g3203015	4243	4532	18	235983.6.dec	3687818H1	3194	3489
18	235983.6.dec	1565654H1	4243	4386	18	235983.6.dec	5865911H1	3196	3467
18	235983.6.dec	g1379563	4243	4533	18	235983.6.dec	5676145H1	3221	3457
18	235983.6.dec	g3191370	4243	4532	18	235983.6.dec	g1691481	3230	3594
18	235983.6.dec	g3233027	4243	4533	18	235983.6.dec	2225035H1	3254	3490
18	235983.6.dec	g29057	4251	4539	18	235983.6.dec	157436H1	3265	3476
18	235983.6.dec	g5108814	4249	4535	18	235983.6.dec	157436R1	3267	3781
18	235983.6.dec	2126663H1	4254	4523	18	235983.6.dec	g2069871	3277	3638
18	235983.6.dec	g1101555	4254	4533	18	235983.6.dec	4445787H1	3278	3515
18	235983.6.dec	1677718H1	4257	4498	18	235983.6.dec	3616513H1	3310	3614
18	235983.6.dec	g877366	4257	4541	18	235983.6.dec	158334H1	3315	3482
18	235983.6.dec	g842556	4256	4533	18	235983.6.dec	726102H1	3614	3838
18	235983.6.dec	g1011570	4258	4546	18	235983.6.dec	1319351H1	3319	3542
18	235983.6.dec	g1039989	4267	4542	18	235983.6.dec	4447125H1	3349	3621
18	235983.6.dec	g2821823	4265	4549	18	235983.6.dec	4648142H1	3358	3618
18	235983.6.dec	g3116989	4265	4539	18	235983.6.dec	3895241H1	3361	3524
18	235983.6.dec	g782426	4269	4547	18	235983.6.dec	2022857H1	3364	3589
18	235983.6.dec	g1939717	4269	4546	18	235983.6.dec	5013742H1	3362	3632
18	235983.6.dec	g2841416	4267	4522	18	235983.6.dec	3407443H1	3369	3605
18	235983.6.d c	g4511390	4270	4533	18	235983.6.dec	1427630F6	3380	3949
18	235983.6.dec	g2821824	4280	4553	18	235983.6.dec	1427630H1	3380	3603
18	235983.6.dec	536291H1	4274	4521	18	235983.6.dec	4890434H1	3388	3568
18	235983.6.dec	g3802343	4276	4541	18	235983.6.dec	g705111	3390	3451
18	235983.6.dec	744021R1	4277	4533	18	235983.6.dec	5301717H1	3420	3637
18	235983.6.dec	744021H1	4277	4517	18	235983.6.dec	1831110H1	3420	3670
18	235983.6.dec	g1727350	4280	4544	18	235983.6.dec	1220017H1	3429	3658

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18	235983.6.dec	3617263H1	1439	1569
18	235983.6.d c	6292515H1	1441	1611
18	235983.6.d c	6289496H1	1444	1611
18	235983.6.dec	5636916H1	1449	1715
18	235983.6.d c	6355532H1	1468	1675
18	235983.6.dec	4070803H1	1491	1776
18	235983.6.dec	4153164H1	1501	1769
18	235983.6.dec	g2810741	1508	1908
18	235983.6.dec	g2901231	1508	1906
18	235983.6.dec	g3050079	1527	1586
18	235983.6.dec	6286265H2	1618	2065
18	235983.6.dec	6284160H1	1618	1861
18	235983.6.dec	6289955H1	1618	1849
18	235983.6.dec	6290838H1	1618	1895
18	235983.6.dec	6290954H1	1618	1803
18	235983.6.dec	3613944H1	1655	1942
18	235983.6.dec	3154382H1	1724	1809
18	235983.6.dec	3363928H1	1738	1983
18	235983.6.dec	2205748H1	1753	1820
18	235983.6.dec	2205748F6	1754	2136
18	235983.6.dec	g395643	1773	2109
18	235983.6.dec	3075529F6	1807	2345
18	235983.6.dec	3419076F6	1812	2130
18	235983.6.dec	5668869H1	1818	2055
18	235983.6.dec	4670760H1	1849	2104
18	235983.6.dec	928449H1	1870	2132
18	235983.6.dec	928449R1	1871	2315
18	235983.6.dec	928449R6	1871	2323
18	235983.6.dec	3492637H1	1918	2181
18	235983.6.dec	484275R6	1990	2490
18	235983.6.dec	484275H1	1990	2231
18	235983.6.dec	g1312232	3851	4278
18	235983.6.dec	g870634	3856	4234
18	235983.6.dec	841880R1	3866	4317
18	235983.6.dec	598558H1	3862	4092
18	235983.6.dec	607754H1	3865	4120
18	235983.6.dec	841880H1	3866	4096
18	235983.6.dec	g2139402	3879	4302
18	235983.6.dec	g2205778	3879	4217
18	235983.6.dec	g2148308	3887	4532
18	235983.6.dec	g781601	3893	4158
18	235983.6.dec	1629908H1	3896	4008
18	235983.6.dec	g4152316	3899	4215
18	235983.6.dec	157436F1	3906	4533
18	235983.6.dec	1613778H1	3906	4121
18	235983.6.dec	g915726	3917	4093
18	235983.6.dec	1427630T6	3920	4503
18	235983.6.dec	g2538933	3924	4224
18	235983.6.dec	4126036H1	3925	4139
18	235983.6.dec	1642393T6	3924	4496
18	235983.6.dec	2525583T6	3931	4495
18	235983.6.dec	1908249T6	3931	4495
18	235983.6.dec	3075529T6	3940	4509
18	235983.6.dec	2608473T6	3947	4500
18	235983.6.dec	6115730H1	3947	4217
18	235983.6.dec	3987442H1	3957	4217
18	235983.6.dec	g842555	3963	4319
18	235983.6.dec	g866443	3963	4262
18	235983.6.dec	2205748T6	3970	4503
18	235983.6.dec	5372056H1	3978	4202
18	235983.6.dec	g5662713	3978	4224
18	235983.6.dec	2420244H1	3978	4197
18	235983.6.dec	5115777H1	3981	4232
18	235983.6.dec	2153213H1	3982	4210
18	235983.6.dec	634825R6	3982	4533
18	235983.6.dec	634825T6	3982	4502
18	235983.6.dec	2153213F6	3982	4498
18	235983.6.dec	1903691H1	3982	4233
18	235983.6.dec	1919746H1	3982	4225
18	235983.6.dec	2853362H1	3982	4217
18	235983.6.dec	634825H1	3982	4217
18	235983.6.d c	g1386214	3986	4423
18	235983.6.dec	3636983T6	3991	4510
18	235983.6.dec	2800978H1	3990	4217
18	235983.6.dec	2554512H1	3990	4217
18	235983.6.dec	4194107H1	3996	4217
18	235983.6.dec	1675942T6	4013	4495
18	235983.6.dec	4803139H1	4015	4225
18	235983.6.dec	5077446H2	4015	4304
18	235983.6.dec	3807695H1	4014	4217
18	235983.6.dec	2243401H1	4020	4203
18	235983.6.dec	1701425H1	4030	4223
18	235983.6.dec	3614535H1	4050	4340
18	235983.6.dec	g1492972	4053	4225
18	235983.6.dec	4742415H1	4054	4306
18	235983.6.dec	816546T1	4056	4546
18	235983.6.dec	816546H1	4056	4344
18	235983.6.dec	g2466524	4060	4542
18	235983.6.dec	4456437H1	4066	4321
18	235983.6.dec	1006262H1	4074	4351
18	235983.6.dec	3014262H1	4070	4365
18	235983.6.dec	g1678520	4074	4544
18	235983.6.dec	2153213T6	4077	4494
18	235983.6.dec	4637011H1	4077	4338
18	235983.6.dec	g2051375	4079	4548
18	235983.6.dec	g5439112	4079	4534
18	235983.6.dec	g3601078	4079	4533
18	235983.6.dec	g5425654	4080	4540
18	235983.6.dec	3015678H1	4080	4361
18	235983.6.dec	3575368H1	4080	4389
18	235983.6.dec	2645890H1	4082	4342
18	235983.6.dec	g4899643	4083	4534
18	235983.6.dec	g3644584	4086	4535
18	235983.6.dec	g2354450	4087	4534
18	235983.6.dec	g4568273	4089	4539
18	235983.6.dec	g5674002	4091	4538
18	235983.6.dec	g3423209	4092	4538
18	235983.6.dec	g2568445	4091	4538
18	235983.6.dec	355120H1	4094	4297
18	235983.6.dec	3586619T6	4100	4513
18	235983.6.dec	484275T6	4101	4503
18	235983.6.dec	g4224047	4104	4546
18	235983.6.dec	g1970154	4107	4431
18	235983.6.dec	g4649188	4110	4533
18	235983.6.dec	g3959037	4124	4537
18	235983.6.dec	g3693698	4124	4533
18	235983.6.dec	g4568110	4124	4533
18	235983.6.dec	g4392393	4125	4541
18	235983.6.dec	g4088342	4127	4548
18	235983.6.dec	4221987H1	4126	4404
18	235983.6.dec	4221393H1	4126	4412
18	235983.6.dec	g4389669	4128	4544
18	235983.6.dec	g4301116	4128	4539
18	235983.6.dec	g4111965	4135	4541
18	235983.6.dec	g2337573	4143	4536
18	235983.6.dec	g3805021	4145	4533
18	235983.6.dec	2641210T6	4149	4494
18	235983.6.dec	g821961	4155	4552
18	235983.6.dec	g2139306	4149	4547
18	235983.6.dec	g2112828	4150	4544
18	235983.6.dec	g2987138	4150	4542
18	235983.6.dec	g4971580	4156	4533
18	235983.6.dec	5279780H1	4157	4389
18	235983.6.dec	g3178678	4157	4539
18	235983.6.dec	g615559	4157	4541
18	235983.6.dec	g615366	4157	4541

Table 2 cont.

19	238703.2.dec	1314852H1	901	1144	19	238703.2.dec	g5526630	1096	1476
19	238703.2.dec	2508937H1	901	1120	19	238703.2.dec	g1614392	1094	1441
19	238703.2.dec	1548794H1	902	1104	19	238703.2.dec	2448115T6	1098	1431
19	238703.2.dec	1734650H1	903	1123	19	238703.2.dec	5683758H1	1102	1337
19	238703.2.d c	1006219H1	908	1135	19	238703.2.dec	g3754298	1110	1473
19	238703.2.dec	2042824H1	911	1055	19	238703.2.dec	5924675H1	1113	1398
19	238703.2.dec	5714657H1	919	1192	19	238703.2.dec	g1761859	1117	1463
19	238703.2.dec	941045R1	934	1443	19	238703.2.dec	g831652	1122	1489
19	238703.2.dec	941045H1	934	1232	19	238703.2.dec	g3988454	1122	1476
19	238703.2.dec	225305H1	950	1126	19	238703.2.dec	g1141926	1124	1471
19	238703.2.dec	225305R1	950	1471	19	238703.2.dec	g1615980	1127	1479
19	238703.2.dec	6269825H1	950	1470	19	238703.2.dec	g3280478	1124	1474
19	238703.2.dec	3097424H1	960	1256	19	238703.2.dec	g3400360	1128	1478
19	238703.2.dec	602414H1	960	1032	19	238703.2.dec	g1801195	1124	1441
19	238703.2.dec	4635313H1	962	1205	19	238703.2.dec	2400926H1	1126	1334
19	238703.2.dec	5597519H1	964	1155	19	238703.2.dec	g4853169	1129	1476
19	238703.2.dec	1688380H1	969	1193	19	238703.2.dec	g2913692	1129	1475
19	238703.2.dec	1688027H1	969	1181	19	238703.2.dec	g4900876	1135	1471
19	238703.2.dec	4800888H1	969	1216	19	238703.2.dec	g653486	1138	1425
19	238703.2.dec	4800701H1	925	1181	19	238703.2.dec	g518075	1133	1471
19	238703.2.dec	4321584H1	976	1248	19	238703.2.dec	g3174834	1137	1470
19	238703.2.dec	1754493H1	978	1203	19	238703.2.dec	g819357	1139	1472
19	238703.2.dec	892038H1	991	1110	19	238703.2.dec	g5177747	1144	1475
19	238703.2.dec	1317383H1	995	1236	19	238703.2.dec	889148H1	1145	1283
19	238703.2.dec	4187641H1	1001	1266	19	238703.2.dec	2345333H1	1150	1406
19	238703.2.dec	g3181350	1001	1471	19	238703.2.dec	g3240653	1157	1479
19	238703.2.dec	g2434396	1001	1448	19	238703.2.dec	g3240758	1157	1479
19	238703.2.dec	g1330862	1008	1481	19	238703.2.dec	g2942603	1162	1471
19	238703.2.dec	g4486259	1007	1405	19	238703.2.dec	g1761875	1162	1475
19	238703.2.dec	4663892H1	1007	1243	19	238703.2.dec	6539614H1	1166	1471
19	238703.2.dec	6324675H1	1011	1308	19	238703.2.dec	g2056722	1166	1481
19	238703.2.dec	g2216083	1014	1471	19	238703.2.dec	5271589H1	1170	1406
19	238703.2.dec	g4486257	1017	1475	19	238703.2.dec	g857757	1168	1449
19	238703.2.dec	g5637989	1020	1482	19	238703.2.dec	g3919555	1169	1585
19	238703.2.dec	g4005327	1020	1472	19	238703.2.dec	g878530	1173	1473
19	238703.2.dec	4552389H1	1018	1137	19	238703.2.dec	g517836	1173	1471
19	238703.2.dec	2046913H1	1024	1166	19	238703.2.dec	5941977H1	1174	1447
19	238703.2.dec	1380073H1	1031	1294	19	238703.2.dec	g3931604	1208	1478
19	238703.2.dec	g3601039	1029	1472	19	238703.2.dec	1865544T6	1208	1433
19	238703.2.dec	g3595709	1030	1477	19	238703.2.dec	g2957926	1221	1474
19	238703.2.dec	g2783614	1032	1475	19	238703.2.dec	g768855	1222	1475
19	238703.2.dec	g3601297	1034	1477	19	238703.2.dec	g690945	1225	1473
19	238703.2.dec	g3840409	1037	1481	19	238703.2.dec	g890047	1234	1471
19	238703.2.dec	g3446295	1046	1475	19	238703.2.dec	g5636513	1235	1476
19	238703.2.dec	g1721081	1047	1476	19	238703.2.dec	g504660	1244	1478
19	238703.2.dec	g2873475	1044	1471	19	238703.2.dec	g1055807	1249	1470
19	238703.2.dec	419939F1	1053	1475	19	238703.2.dec	g884483	1251	1464
19	238703.2.dec	g2675501	1054	1479	19	238703.2.dec	g2932400	1255	1476
19	238703.2.dec	g2464041	1053	1477	19	238703.2.dec	g4649715	1269	1472
19	238703.2.dec	419939R1	1055	1475	19	238703.2.dec	g760527	1273	1471
19	238703.2.dec	419939H1	1055	1254	19	238703.2.dec	g2433575	1270	1471
19	238703.2.dec	5555467H1	1059	1319	19	238703.2.dec	g3840266	1276	1481
19	238703.2.dec	g3841172	1060	1475	19	238703.2.dec	g3056119	1277	1479
19	238703.2.dec	1703942H1	1059	1278	19	238703.2.dec	g751598	1276	1471
19	238703.2.dec	g2874018	1063	1475	19	238703.2.dec	959656H1	1276	1587
19	238703.2.dec	508789H1	1066	1268	19	238703.2.dec	g919116	1277	1413
19	238703.2.dec	3804783H1	1068	1378	19	238703.2.dec	1858793T6	1289	1426
19	238703.2.dec	3454454H2	1072	1338	19	238703.2.dec	1573709H1	1290	1471
19	238703.2.dec	2918331H1	1071	1352	19	238703.2.dec	6194016H1	1296	1476
19	238703.2.dec	4416076H1	1075	1309	19	238703.2.dec	1858793H1	1296	1471
19	238703.2.dec	5161427H2	1076	1316	19	238703.2.dec	1858793F6	1296	1413
19	238703.2.dec	g696501	1091	1475	19	238703.2.dec	g2359502	1304	1471
19	238703.2.dec	g1259095	1082	1407	19	238703.2.dec	g5540475	1302	1474
19	238703.2.dec	6380782H1	1087	1342	19	238703.2.dec	g3765011	1302	1474
19	238703.2.dec	1856905H1	1089	1361	19	238703.2.dec	g2767462	1308	1471
19	238703.2.dec	g5127944	1092	1471	19	238703.2.dec	g2004475	1310	1645
19	238703.2.dec	g680899	1103	1462	19	238703.2.dec	941777H1	1335	1471
19	238703.2.dec	g3884338	1095	1479	19	238703.2.dec	940928T1	1335	1428

Table 2 cont.

18	235983.6.dec	946064H1	3433	3663
18	235983.6.dec	1506434H1	3436	3640
18	235983.6.dec	1450559F1	3452	3849
18	235983.6.dec	2216623H1	3452	3691
18	235983.6.dec	1450559H1	3452	3724
18	235983.6.dec	3661936H1	3454	3721
18	235983.6.dec	4057520H1	3462	3592
18	235983.6.dec	6600083H1	3461	3978
18	235983.6.dec	6212917H1	3461	3616
18	235983.6.dec	5576802H1	3473	3724
18	235983.6.dec	4649217H1	3478	3749
18	235983.6.dec	726102R1	3614	4028
18	235983.6.dec	g779370	3485	3826
18	235983.6.dec	6422802H1	3486	4001
18	235983.6.dec	1735285H1	3485	3696
18	235983.6.dec	4649317H1	3488	3755
18	235983.6.dec	g2114721	3488	3882
18	235983.6.dec	2382364H1	3491	3724
18	235983.6.dec	g1157467	3498	3877
18	235983.6.dec	g2013827	3503	3727
18	235983.6.dec	2289250H1	3510	3734
18	235983.6.dec	4355633H1	3517	3655
18	235983.6.dec	g877365	3517	3723
18	235983.6.dec	045305H1	3522	3667
18	235983.6.dec	5733071H1	3545	3799
18	235983.6.dec	3636983F6	3547	4117
18	235983.6.dec	3637383H1	3547	3809
18	235983.6.dec	4062466H1	3555	3828
18	235983.6.dec	1367637R1	3558	4072
18	235983.6.dec	1367637H1	3558	3800
18	235983.6.dec	g29058	3575	3911
18	235983.6.dec	g1792226	3580	4005
18	235983.6.dec	821700H1	3616	3866
18	235983.6.dec	1908249F6	3588	4139
18	235983.6.dec	3223615H1	3594	3901
18	235983.6.dec	898523H1	3598	3874
18	235983.6.dec	898523R1	3600	4148
18	235983.6.dec	5575549H1	3600	3774
18	235983.6.dec	4787384H1	3603	3853
18	235983.6.dec	5952613H1	3607	3901
19	238703.2.dec	1451578H1	442	695
19	238703.2.dec	6110523H1	451	758
19	238703.2.dec	6602392H1	459	915
19	238703.2.dec	g2216250	462	901
19	238703.2.dec	g690552	469	736
19	238703.2.dec	4622639H1	469	723
19	238703.2.dec	g690544	470	734
19	238703.2.dec	3873078H1	470	752
19	238703.2.dec	2651203H1	469	719
19	238703.2.dec	4173688H1	469	754
19	238703.2.dec	g612081	469	746
19	238703.2.dec	6370323H1	485	991
19	238703.2.dec	1564889H1	489	581
19	238703.2.dec	1539071H1	490	701
19	238703.2.dec	2529509H1	501	827
19	238703.2.dec	g1330918	507	1037
19	238703.2.dec	851725H1	511	771
19	238703.2.dec	852289H1	511	751
19	238703.2.dec	g613245	513	838
19	238703.2.dec	158598H1	520	785
19	238703.2.dec	879281R1	526	1092
19	238703.2.dec	046054H1	526	831
19	238703.2.dec	1542430H1	528	940
19	238703.2.dec	879281H1	526	770
19	238703.2.dec	3162910H1	560	860
19	238703.2.dec	3297858H1	573	831
19	238703.2.dec	1570087H1	581	787
19	238703.2.dec	1572130H1	581	770
19	238703.2.d c	g1810435	583	950
19	238703.2.dec	6166895H1	592	1125
19	238703.2.dec	4767523H1	592	748
19	238703.2.dec	2590909H1	616	907
19	238703.2.dec	5854491H1	622	896
19	238703.2.dec	g696662	628	963
19	238703.2.dec	g760902	628	846
19	238703.2.dec	g685255	628	915
19	238703.2.dec	g861831	630	732
19	238703.2.dec	5272964H1	630	805
19	238703.2.dec	5173648H1	650	926
19	238703.2.dec	2071937H1	651	898
19	238703.2.dec	4512283H1	654	914
19	238703.2.dec	2307229H1	665	926
19	238703.2.dec	4460408H1	665	925
19	238703.2.dec	537008H1	672	771
19	238703.2.dec	6385387H1	676	960
19	238703.2.dec	6382968H1	676	905
19	238703.2.dec	5846001H1	681	889
19	238703.2.dec	3223621H1	702	1006
19	238703.2.dec	2933878H1	707	968
19	238703.2.dec	5303446H1	707	952
19	238703.2.dec	g985999	709	1074
19	238703.2.dec	2913208H1	709	968
19	238703.2.dec	g751597	713	979
19	238703.2.dec	g760618	713	983
19	238703.2.dec	4199245H1	714	980
19	238703.2.dec	1341926F6	716	1236
19	238703.2.dec	1338691H1	716	996
19	238703.2.dec	1341931H1	716	807
19	238703.2.dec	1338791H1	716	953
19	238703.2.dec	2570052H1	719	921
19	238703.2.dec	5667719H1	748	998
19	238703.2.dec	2724240H1	749	991
19	238703.2.dec	4527637H1	768	1014
19	238703.2.dec	1608241H1	772	968
19	238703.2.dec	3713108H1	775	1066
19	238703.2.dec	2544621H1	785	1027
19	238703.2.dec	857987H1	786	1038
19	238703.2.dec	4855630H1	800	1064
19	238703.2.dec	1507116H1	799	1019
19	238703.2.dec	6011557H1	815	1086
19	238703.2.dec	6011657H1	815	1082
19	238703.2.dec	g918677	816	1097
19	238703.2.dec	g824402	816	1160
19	238703.2.dec	1896158H1	825	1075
19	238703.2.dec	4361273H1	825	1068
19	238703.2.dec	g1044402	826	1151
19	238703.2.dec	2506071H1	831	1009
19	238703.2.dec	2041150H1	843	1110
19	238703.2.dec	2359650H1	850	1115
19	238703.2.dec	1750967H1	851	1079
19	238703.2.dec	g878583	859	1156
19	238703.2.dec	4972424H1	861	1026
19	238703.2.dec	1242092H1	861	995
19	238703.2.dec	4608277H1	865	1122
19	238703.2.dec	g1524467	867	1026
19	238703.2.dec	2696178H1	870	1168
19	238703.2.dec	169710H1	874	1107
19	238703.2.dec	171492H1	874	1088
19	238703.2.dec	3244540H1	890	1124
19	238703.2.d c	889000R1	890	1456
19	238703.2.d c	889000H1	890	1158
19	238703.2.dec	2213805H1	891	1111
19	238703.2.dec	722196H1	893	1153
19	238703.2.dec	g1383346	895	1331
19	238703.2.d c	4546493H1	901	1162
19	238703.2.dec	942202H1	900	1029

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19	238703.2.dec	g2752558	1184	1475	20	038751.5.dec	4649238H1	381	652
19	238703.2.dec	g1735144	1192	1475	20	038751.5.dec	1432680R1	416	909
19	238703.2.dec	1727979H1	1201	1260	20	038751.5.dec	1432680H1	416	681
19	238703.2.dec	1922139H1	1201	1459	20	038751.5.dec	5028237H1	421	526
20	038751.5.dec	5891158H1	1053	1324	20	038751.5.dec	3735509H1	428	653
20	038751.5.dec	5884165H1	1053	1309	20	038751.5.dec	g944693	457	759
20	038751.5.dec	g2115213	1054	1513	20	038751.5.dec	4441762H1	463	594
20	038751.5.dec	2073762H1	1056	1303	20	038751.5.dec	6599874H1	491	985
20	038751.5.dec	4516520H1	1059	1307	20	038751.5.dec	g1625374	526	843
20	038751.5.dec	2058487H1	1082	1333	20	038751.5.dec	874318R1	530	1138
20	038751.5.dec	g5364468	1107	1573	20	038751.5.dec	874318H1	530	816
20	038751.5.dec	2058968H1	1113	1371	20	038751.5.dec	1692115F6	532	938
20	038751.5.dec	g3665026	1126	1570	20	038751.5.dec	1692115H1	532	749
20	038751.5.dec	g5110105	1129	1563	20	038751.5.dec	3189812H1	540	858
20	038751.5.dec	5951458H1	1141	1451	20	038751.5.dec	3838242H1	548	828
20	038751.5.dec	1731310T6	1146	1449	20	038751.5.dec	2701789H1	562	739
20	038751.5.dec	g4328520	1156	1566	20	038751.5.dec	6615168H1	597	1145
20	038751.5.dec	g657692	1170	1561	20	038751.5.dec	275704H1	600	771
20	038751.5.dec	287003H1	1157	1516	20	038751.5.dec	653895H1	610	847
20	038751.5.dec	6077974H1	1160	1402	20	038751.5.dec	5562625H1	619	836
20	038751.5.dec	6506745H1	1185	1542	20	038751.5.dec	2061473H1	655	923
20	038751.5.dec	6506945H1	1185	1542	20	038751.5.dec	2528543H1	673	973
20	038751.5.dec	3705392H1	1186	1478	20	038751.5.dec	4311336H1	684	1005
20	038751.5.dec	g3895500	1191	1567	20	038751.5.dec	1731310F6	684	1026
20	038751.5.dec	g4329793	1193	1569	20	038751.5.dec	1731310H1	684	908
20	038751.5.dec	g4078804	1199	1570	20	038751.5.dec	4379489H1	695	966
20	038751.5.dec	g2840648	1199	1566	20	038751.5.dec	5317556H1	780	1037
20	038751.5.dec	g2114887	1201	1573	20	038751.5.dec	5316328H1	780	995
20	038751.5.dec	g5368723	1207	1574	20	038751.5.dec	5315861H1	780	931
20	038751.5.dec	g1625271	1207	1566	20	038751.5.dec	5883926H1	847	1111
20	038751.5.dec	g4076938	1213	1571	20	038751.5.dec	5884301H1	847	1103
20	038751.5.dec	g698323	1234	1572	20	038751.5.dec	2351121F6	852	1223
20	038751.5.dec	g2779516	1239	1543	20	038751.5.dec	2348432H1	852	1085
20	038751.5.dec	1692115T6	1244	1529	20	038751.5.dec	2351121H1	852	1067
20	038751.5.dec	g4524126	1246	1570	20	038751.5.dec	g1512998	856	1323
20	038751.5.dec	g4453022	1250	1560	20	038751.5.dec	4665163H1	861	1124
20	038751.5.dec	g2212328	1252	1566	20	038751.5.dec	1427102H1	861	1095
20	038751.5.dec	g3896194	1286	1571	20	038751.5.dec	085427H1	874	1061
20	038751.5.dec	g788314	1321	1569	20	038751.5.dec	5177489H1	885	1154
20	038751.5.dec	g723868	1338	1568	20	038751.5.dec	g657742	910	1134
20	038751.5.dec	g718978	1346	1570	20	038751.5.dec	g4982887	911	1374
20	038751.5.dec	g846280	1348	1546	20	038751.5.dec	1482576H1	923	1154
20	038751.5.dec	g1955112	1363	1566	20	038751.5.dec	1005907H1	931	1262
20	038751.5.dec	g1512999	1365	1580	20	038751.5.dec	3700251H1	951	1258
20	038751.5.dec	2109081H1	1369	1567	20	038751.5.dec	508498H1	963	1170
20	038751.5.dec	g4617986	1388	1570	20	038751.5.dec	1446007H1	967	1207
20	038751.5.dec	3570081H1	1396	1563	20	038751.5.dec	g1512388	971	1451
20	038751.5.dec	1627963H1	1398	1556	20	038751.5.dec	4674472H1	976	1242
20	038751.5.dec	827450H1	1404	1570	20	038751.5.dec	4677451H1	976	1249
20	038751.5.dec	4467140H1	1441	1566	20	038751.5.dec	2872036H1	976	1204
20	038751.5.dec	g3095819	1446	1575	20	038751.5.dec	236814H1	980	1205
20	038751.5.dec	1634593H1	1470	1570	20	038751.5.dec	3986488T6	981	1552
20	038751.5.dec	1635044H1	1470	1574	20	038751.5.dec	4215124H1	987	1274
20	038751.5.dec	1914206H1	1470	1570	20	038751.5.dec	5085815H1	995	1112
20	038751.5.dec	g4223279	1130	1565	20	038751.5.dec	g751557	996	1232
20	038751.5.dec	g1273271	910	1323	20	038751.5.dec	1470940H1	998	1174
20	038751.5.dec	6064949H1	914	1209	20	038751.5.dec	1634141T6	1019	1524
20	038751.5.dec	6298614H1	1	298	20	038751.5.dec	2073596H1	1021	1241
20	038751.5.dec	4726788H1	82	321	20	038751.5.dec	2351121T6	1020	1526
20	038751.5.dec	667079H1	157	391	20	038751.5.dec	2757071H1	1030	1291
20	038751.5.dec	3557951H1	210	476	20	038751.5.dec	1634141F6	1026	1571
20	038751.5.dec	g779810	248	568	20	038751.5.dec	1634141H1	1026	1258
20	038751.5.dec	g4008516	248	1570	21	236099.4.dec	5465756H1	1	288
20	038751.5.dec	2046232H1	307	584	21	236099.4.dec	1622240F6	5	358
20	038751.5.dec	2046232F6	307	607	21	236099.4.dec	1622240H1	5	220
20	038751.5.dec	459067H1	310	561	21	236099.4.dec	582350H1	5	262
20	038751.5.dec	g697893	327	600	21	236099.4.dec	5616026H1	15	285
20	038751.5.dec	g711339	359	603	21	236099.4.dec	6171515H1	15	336

Table 2 cont.

19	238703.2.dec	940928H1	1335	1470
19	238703.2.dec	g2166356	1349	1461
19	238703.2.dec	g3148439	1373	1476
19	238703.2.dec	g3740259	1398	1471
19	238703.2.dec	g1813211	1415	1477
19	238703.2.dec	g2782077	1421	1475
19	238703.2.dec	g3891243	1174	1471
19	238703.2.dec	g1801567	1	85
19	238703.2.dec	4552078H1	1	226
19	238703.2.dec	803067H1	1	219
19	238703.2.dec	423072H1	1	144
19	238703.2.dec	3148690H1	1	272
19	238703.2.dec	3539439H1	1	227
19	238703.2.dec	3586007H1	2	317
19	238703.2.dec	4434676H1	3	277
19	238703.2.dec	3273403H1	5	243
19	238703.2.dec	3772776H1	5	301
19	238703.2.dec	3672353H1	5	199
19	238703.2.dec	492072H1	6	245
19	238703.2.dec	265112R1	12	542
19	238703.2.dec	3335884H1	13	276
19	238703.2.dec	3140272H1	12	294
19	238703.2.dec	265112H1	11	251
19	238703.2.dec	4518884H1	11	227
19	238703.2.dec	2486378H1	16	98
19	238703.2.dec	3449649H1	18	282
19	238703.2.dec	g1713059	25	250
19	238703.2.dec	4383163H1	25	163
19	238703.2.dec	2545859H1	24	280
19	238703.2.dec	3482476H1	26	298
19	238703.2.dec	1865544F6	25	390
19	238703.2.dec	3074630H1	26	300
19	238703.2.dec	1865544H1	25	276
19	238703.2.dec	g1722043	21	293
19	238703.2.dec	482687H1	26	259
19	238703.2.dec	3747723H1	26	228
19	238703.2.dec	4569176H1	29	295
19	238703.2.dec	486383H1	27	266
19	238703.2.dec	1338949H1	28	270
19	238703.2.dec	3216994H1	33	257
19	238703.2.dec	2935963H1	31	118
19	238703.2.dec	485050H1	33	270
19	238703.2.dec	5165752H1	33	280
19	238703.2.dec	484526H1	33	266
19	238703.2.dec	486726H1	33	266
19	238703.2.dec	4152430H1	34	313
19	238703.2.dec	3592529H1	36	347
19	238703.2.dec	3174680H1	36	291
19	238703.2.dec	799668H1	35	269
19	238703.2.dec	3614882H1	36	329
19	238703.2.dec	2809066H1	37	318
19	238703.2.dec	4802648H1	37	297
19	238703.2.dec	2809052H1	36	331
19	238703.2.dec	g1750653	34	381
19	238703.2.dec	4010723H1	39	309
19	238703.2.dec	2445515H1	37	292
19	238703.2.dec	3462802H1	37	186
19	238703.2.dec	4911152H1	38	338
19	238703.2.dec	3358571H1	41	229
19	238703.2.dec	2448115F6	41	391
19	238703.2.dec	2448115H1	41	290
19	238703.2.dec	3538108H1	43	338
19	238703.2.dec	3504412H1	45	353
19	238703.2.dec	g832320	40	472
19	238703.2.dec	g1761858	42	380
19	238703.2.dec	3151580H1	45	326
19	238703.2.dec	4975922H1	45	322
19	238703.2.d c	3273757H1	45	310
19	238703.2.dec	2762734H1	45	296
19	238703.2.dec	2762735F6	45	141
19	238703.2.dec	3082047H1	45	339
19	238703.2.dec	3337993H1	50	290
19	238703.2.dec	2204857H1	50	305
19	238703.2.dec	3271745H1	50	290
19	238703.2.dec	g1055806	46	134
19	238703.2.dec	g1155874	50	383
19	238703.2.dec	2850809H1	54	368
19	238703.2.dec	g1616084	55	381
19	238703.2.dec	g653641	75	240
19	238703.2.dec	g2007777	130	363
19	238703.2.dec	g2056105	129	587
19	238703.2.dec	4522841H1	164	423
19	238703.2.dec	2208971H1	228	475
19	238703.2.dec	g389513	242	656
19	238703.2.dec	4074294H1	261	544
19	238703.2.dec	5585128H1	261	497
19	238703.2.dec	4344148H1	261	478
19	238703.2.dec	g613807	273	546
19	238703.2.dec	g613822	273	540
19	238703.2.dec	g1761874	280	350
19	238703.2.dec	5516366H1	296	421
19	238703.2.dec	080407H1	296	549
19	238703.2.dec	g1735242	302	599
19	238703.2.dec	1932969H1	308	556
19	238703.2.dec	6485648H1	316	845
19	238703.2.dec	1932969F6	308	700
19	238703.2.dec	5810554H1	309	626
19	238703.2.dec	5810747H1	309	634
19	238703.2.dec	5159576H1	317	571
19	238703.2.dec	035462H1	319	593
19	238703.2.dec	039530H1	319	529
19	238703.2.dec	6313127H1	335	867
19	238703.2.dec	g884522	336	675
19	238703.2.dec	033286H1	337	400
19	238703.2.dec	033287H1	343	545
19	238703.2.dec	073634H1	350	540
19	238703.2.dec	073692H1	350	545
19	238703.2.dec	3282162H1	372	628
19	238703.2.dec	4398152H1	372	607
19	238703.2.dec	g616518	378	587
19	238703.2.dec	1834264H1	379	561
19	238703.2.dec	4917182H1	381	594
19	238703.2.dec	187622H1	386	569
19	238703.2.dec	2478077H1	398	631
19	238703.2.dec	2098940H1	404	639
19	238703.2.dec	2488430H1	404	635
19	238703.2.dec	6064576H1	405	700
19	238703.2.dec	5995783H1	405	695
19	238703.2.dec	g1958061	412	842
19	238703.2.dec	g890104	412	540
19	238703.2.dec	4596304H1	412	665
19	238703.2.dec	4597956H1	412	662
19	238703.2.dec	g918642	421	642
19	238703.2.dec	1284283H1	421	635
19	238703.2.dec	4553582H1	423	668
19	238703.2.dec	g1646327	426	781
19	238703.2.dec	4010634H1	434	735
19	238703.2.dec	5992727H1	441	744
19	238703.2.dec	4900130H1	441	704
19	238703.2.dec	1451578F1	442	913
19	238703.2.dec	g851482	1207	1449
19	238703.2.dec	g3648126	1179	1477
19	238703.2.dec	g861832	1177	1470
19	238703.2.dec	889877H1	1181	1411
19	238703.2.dec	g1383298	1184	1486
19	238703.2.d c	g1750539	1181	1478

Table 2 cont.

21	236099.4.dec	6095067H1	19	323	21	236099.4.d c	3251609F6	1097	1514
21	236099.4.dec	4634203H1	19	302	21	236099.4.dec	3251609H1	1097	1401
21	236099.4.dec	532086H1	21	271	21	236099.4.dec	5865657H1	1100	1367
21	236099.4.dec	g2080681	19	376	21	236099.4.dec	2512120T6	1105	1670
21	236099.4.dec	4415334H1	23	287	21	236099.4.dec	5744630H1	1113	1381
21	236099.4.dec	4703802H1	24	207	21	236099.4.dec	g2161810	1118	1554
21	236099.4.dec	6549766H1	25	620	21	236099.4.dec	1600152H1	1137	1343
21	236099.4.dec	3566591H1	25	264	21	236099.4.dec	5605484H1	1156	1430
21	236099.4.dec	1389095H1	25	250	21	236099.4.dec	g2027235	1171	1452
21	236099.4.dec	6008955H1	27	309	21	236099.4.dec	5314568H1	1213	1433
21	236099.4.dec	2070696H1	27	280	21	236099.4.dec	g4260562	1231	1706
21	236099.4.dec	3746033H1	30	283	21	236099.4.dec	4180560T8	1232	1685
21	236099.4.dec	3586436H1	29	222	21	236099.4.dec	g2539107	1236	1709
21	236099.4.dec	3750032H1	30	303	21	236099.4.dec	3805461H1	1240	1547
21	236099.4.dec	2818544H1	33	327	21	236099.4.dec	g2566268	1240	1708
21	236099.4.dec	4762420H1	33	291	21	236099.4.dec	g4982919	1239	1703
21	236099.4.dec	2655186H1	37	328	21	236099.4.dec	2411813H1	1243	1484
21	236099.4.dec	258736H1	39	131	21	236099.4.dec	5302238H2	1247	1500
21	236099.4.dec	945328H1	42	312	21	236099.4.dec	g3417716	1248	1706
21	236099.4.dec	238507R1	45	535	21	236099.4.dec	g4311838	1248	1710
21	236099.4.dec	3219002H1	44	336	21	236099.4.dec	g4085716	1248	1628
21	236099.4.dec	3808753H1	47	351	21	236099.4.dec	1926463R6	1249	1595
21	236099.4.dec	1388805H1	47	293	21	236099.4.dec	6375524H1	1249	1545
21	236099.4.dec	5421931H1	48	300	21	236099.4.dec	g1404330	1248	1691
21	236099.4.dec	238507H1	46	275	21	236099.4.dec	1926463T6	1249	1661
21	236099.4.dec	1003290H1	48	274	21	236099.4.dec	1802927T6	1250	1657
21	236099.4.dec	2698971H1	48	261	21	236099.4.dec	1926463H1	1249	1463
21	236099.4.dec	3148652H1	48	338	21	236099.4.dec	g2194686	1251	1505
21	236099.4.dec	2893513H1	51	325	21	236099.4.dec	g2194934	1251	1444
21	236099.4.dec	5095847H1	54	320	21	236099.4.dec	4058927H1	1256	1530
21	236099.4.dec	6125638H1	53	536	21	236099.4.dec	g5636939	1256	1706
21	236099.4.dec	2457030H1	53	283	21	236099.4.dec	772821H1	1263	1474
21	236099.4.dec	3535276H1	54	344	21	236099.4.dec	238507F1	1272	1699
21	236099.4.dec	3590255H1	54	320	21	236099.4.dec	2239910H1	1275	1483
21	236099.4.dec	6119241H1	65	406	21	236099.4.dec	2603359T6	1280	1669
21	236099.4.dec	6125460H1	65	464	21	236099.4.dec	g2080682	1286	1711
21	236099.4.dec	6119192H1	65	626	21	236099.4.dec	4602424T6	1289	1665
21	236099.4.dec	4194343H1	73	374	21	236099.4.dec	6106532H1	1292	1631
21	236099.4.dec	4158894H1	94	350	21	236099.4.dec	g4261108	1296	1706
21	236099.4.dec	g389440	144	513	21	236099.4.dec	g4223524	1298	1706
21	236099.4.dec	g570803	175	522	21	236099.4.dec	g4109832	1300	1706
21	236099.4.dec	g673306	175	488	21	236099.4.dec	1622240T6	1301	1667
21	236099.4.dec	4908387H1	180	442	21	236099.4.dec	g2161667	1311	1709
21	236099.4.dec	641175H1	225	469	21	236099.4.dec	g3432780	1309	1706
21	236099.4.dec	3790670H1	278	569	21	236099.4.dec	g2350629	1312	1706
21	236099.4.dec	5268416H1	316	569	21	236099.4.dec	g3898751	1316	1706
21	236099.4.dec	3589959H1	375	703	21	236099.4.dec	g4524466	1319	1699
21	236099.4.dec	4190221H1	397	676	21	236099.4.dec	g5177660	1319	1696
21	236099.4.dec	3967058H1	408	691	21	236099.4.dec	4842322H1	1321	1602
21	236099.4.dec	1427256F6	502	1075	21	236099.4.dec	g2194974	1322	1699
21	236099.4.dec	1427256H1	502	737	21	236099.4.dec	5486490H1	1324	1599
21	236099.4.dec	5386176H1	528	657	21	236099.4.dec	g3015825	1347	1712
21	236099.4.dec	1718014H1	655	897	21	236099.4.dec	4402183H1	1356	1611
21	236099.4.dec	4010711H1	678	949	21	236099.4.dec	g5674364	1357	1707
21	236099.4.dec	6542821H1	777	1331	21	236099.4.dec	g4153286	1360	1699
21	236099.4.dec	5492621H1	894	1166	21	236099.4.dec	3411727H1	1368	1626
21	236099.4.dec	5492721H1	894	1164	21	236099.4.dec	g2194722	1381	1699
21	236099.4.dec	6256961H1	910	1160	21	236099.4.dec	g4853341	1391	1706
21	236099.4.dec	5979837H1	946	1230	21	236099.4.dec	g4111480	1401	1707
21	236099.4.dec	5273408H1	983	1239	21	236099.4.dec	g5234565	1403	1705
21	236099.4.dec	3163001H1	994	1276	21	236099.4.dec	501997H1	1406	1617
21	236099.4.dec	g2032366	994	1273	21	236099.4.dec	6350508H2	1409	1706
21	236099.4.dec	6308691H1	1006	1558	21	236099.4.d c	6366728H1	1415	1682
21	236099.4.dec	g2743130	1035	1393	21	236099.4.d c	g2715316	1418	1706
21	236099.4.dec	5554939H1	1061	1304	21	236099.4.d c	2365285H1	1433	1661
21	236099.4.dec	1427256T6	1088	1660	21	236099.4.dec	2365114H1	1433	1660
21	236099.4.dec	5224984H1	1093	1335	21	236099.4.dec	2686807H1	1439	1699
21	236099.4.dec	5560308H1	1096	1332	21	236099.4.dec	3168773H1	1441	1705

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21	236099.4.d c	g1389204	1442	1850
21	236099.4.dec	g1626758	1468	1650
21	236099.4.dec	2750215H1	1486	1695
21	236099.4.d c	3950250H1	1492	1680
21	236099.4.dec	g3842605	1498	1699
21	236099.4.dec	g2705688	1503	1983
21	236099.4.dec	g3191411	1505	1706
21	236099.4.dec	g1990989	1508	1706
21	236099.4.dec	942018H1	1513	1706
21	236099.4.dec	942018T1	1513	1668
21	236099.4.dec	942018R1	1513	1706
21	236099.4.dec	6409055H1	1519	1725
21	236099.4.dec	1377067F1	1531	1711
21	236099.4.dec	4784982H2	1532	1699
21	236099.4.dec	g2539580	1535	1699
21	236099.4.dec	g2782664	1559	1930
21	236099.4.dec	g4567742	1581	1706
21	236099.4.dec	2151758H1	1585	1857
21	236099.4.dec	1733668H1	1588	1706
21	236099.4.dec	1733668F6	1588	1706
21	236099.4.dec	g2816105	1602	1992
21	236099.4.dec	g1391414	1627	1983
21	236099.4.dec	5028373H1	1634	1699
21	236099.4.dec	g1404224	1635	1983
21	236099.4.dec	g562487	1682	1983
21	236099.4.dec	g670491	1701	1983
21	236099.4.dec	501104H1	1782	1975
22	350875.2.dec	3338230H1	1	201
22	350875.2.dec	269145H1	1	308
22	350875.2.dec	3641204H1	8	222
22	350875.2.dec	2324423R6	15	473
22	350875.2.dec	2324423H1	15	234
22	350875.2.dec	939129R1	19	366
22	350875.2.dec	6272936H1	20	465
22	350875.2.dec	939129T1	19	424
22	350875.2.dec	939129H1	19	190
22	350875.2.dec	1387573H1	22	234
22	350875.2.dec	1388318H1	22	150
22	350875.2.dec	3535330H1	26	330
22	350875.2.dec	g1995966	32	344
22	350875.2.dec	g1138500	44	344
22	350875.2.dec	g4622245	54	467
22	350875.2.dec	3852439H1	56	329
22	350875.2.dec	2432882H1	90	319
22	350875.2.dec	4790250H1	273	536
22	350875.2.dec	2207794F6	466	1028
22	350875.2.dec	2207794H1	466	735
22	350875.2.dec	4112486H1	577	842
22	350875.2.dec	5095324H1	824	1085
23	466521.5.dec	066981H1	1	184
23	466521.5.dec	792784R1	25	620
23	466521.5.dec	792784H1	25	258
23	466521.5.dec	g1389437	111	529
23	466521.5.dec	4999811H1	127	416
23	466521.5.dec	4999820H1	128	415
23	466521.5.dec	4999825H1	128	415
23	466521.5.dec	6045673H1	144	618
23	466521.5.dec	6045673J1	144	618
23	466521.5.dec	4550289T1	175	676
23	466521.5.dec	066981T6	225	673
23	466521.5.dec	1457775H1	272	523
23	466521.5.dec	g3595167	273	721
23	466521.5.dec	g3678473	341	719
23	466521.5.dec	g3076927	374	710
23	466521.5.dec	g1395834	382	713
23	466521.5.dec	g2955287	388	712
24	466521.6.dec	2345057H1	3	257
24	466521.6.dec	4788225H1	1	213
24	466521.6.dec	4550289H1	1	249
24	466521.6.dec	6141654H1	1	262
24	466521.6.dec	2345057F6	3	409
24	466521.6.dec	g1068909	8	332
24	466521.6.dec	4092590H1	8	270
24	466521.6.dec	3636049H1	9	209
24	466521.6.dec	4951479H2	10	276
24	466521.6.dec	5843619H1	10	243
24	466521.6.dec	922794H1	12	329
24	466521.6.dec	3880786H1	12	289
24	466521.6.dec	6254665H1	16	266
24	466521.6.dec	4399286H1	19	284
24	466521.6.dec	g2008042	20	329
24	466521.6.dec	4746824H2	29	312
24	466521.6.dec	737364H1	30	269
24	466521.6.dec	3439046H1	38	216
24	466521.6.dec	3359046H1	48	307
24	466521.6.dec	105101H1	49	249
24	466521.6.dec	4976429H1	51	309
24	466521.6.dec	2345057T6	295	796
24	466521.6.dec	3871819T6	447	799
24	466521.6.dec	4839970H1	451	736
24	466521.6.dec	3358415H1	491	764
24	466521.6.dec	5549503H1	493	739
24	466521.6.dec	5549567H1	495	732
24	466521.6.dec	905771H1	496	598
24	466521.6.dec	1208881H1	649	834
24	466521.6.dec	1208881R1	649	834
24	466521.6.dec	1208881T1	649	797
24	466521.6.dec	2535788H1	690	834
24	466521.6.dec	2424602H1	690	834
24	466521.6.dec	3133389H1	690	834
24	466521.6.dec	5154535H1	690	834
24	466521.6.dec	5027483H1	704	834
24	466521.6.dec	5027393H1	704	834
24	466521.6.dec	2501570H1	719	834
24	466521.6.dec	2493474H1	719	834
24	466521.6.dec	3729233T1	732	792
24	466521.6.dec	3729291T1	732	792
24	466521.6.dec	3729261T1	732	792
24	466521.6.dec	2058270H1	738	974
24	466521.6.dec	3729264H1	739	834
24	466521.6.dec	5261576H1	746	822
24	466521.6.dec	g2619476	749	834
24	466521.6.dec	g2955142	752	834
24	466521.6.dec	938180R1	769	834
25	474522.8.dec	1702155H1	489	702
25	474522.8.dec	799262H1	505	754
25	474522.8.dec	6160402H1	526	826
25	474522.8.dec	g1971042	537	818
25	474522.8.dec	6023644H1	583	857
25	474522.8.dec	631782H1	614	915
25	474522.8.dec	2201893H1	619	846
25	474522.8.dec	2437919H1	621	856
25	474522.8.dec	3645543H1	625	902
25	474522.8.dec	g2195711	633	928
25	474522.8.dec	3435517H1	644	888
25	474522.8.dec	g1525870	643	1018
25	474522.8.dec	961248H1	665	810
25	474522.8.dec	825000R1	678	1222
25	474522.8.dec	825000H1	678	976
25	474522.8.dec	g783187	690	904
25	474522.8.dec	1805615H1	690	956
25	474522.8.dec	4287472H1	691	887
25	474522.8.dec	3108601H1	693	863
25	474522.8.dec	6060467H1	700	1291
25	474522.8.dec	6264353H1	708	1290
25	474522.8.dec	4246633H1	707	986

Table 2 cont.

25	474522.8.dec	4540246H1	733	907	25	474522.8.dec	4934454H1	74	348
25	474522.8.dec	5855717H1	744	1027	25	474522.8.dec	6343136H1	97	371
25	474522.8.dec	2916788H1	766	1032	25	474522.8.dec	3297190H1	105	348
25	474522.8.dec	5575857H1	765	958	25	474522.8.dec	g3742336	1	390
25	474522.8.dec	6132989H1	778	992	25	474522.8.dec	g3415484	1	284
25	474522.8.dec	g1509952	781	970	25	474522.8.dec	g4188698	1	253
25	474522.8.dec	1358904T6	829	1408	25	474522.8.dec	g2003036	1	375
25	474522.8.dec	1643034F6	837	1404	25	474522.8.dec	g3923493	1	413
25	474522.8.dec	1643034H1	837	1062	25	474522.8.dec	3741633H1	1	285
25	474522.8.dec	3013573H1	847	1131	25	474522.8.dec	6397326H1	9	300
25	474522.8.dec	3683622H1	851	1148	25	474522.8.dec	g5395341	12	454
25	474522.8.dec	1623584H1	849	1068	25	474522.8.dec	2497236F6	16	475
25	474522.8.dec	1972573H1	852	1119	25	474522.8.dec	2497236F7	16	365
25	474522.8.dec	6304864H1	853	1418	26	231583.3.dec	g2898638	900	1195
25	474522.8.dec	1346231H1	855	1069	26	231583.3.dec	g1858640	907	1261
25	474522.8.dec	1489583H1	869	1130	26	231583.3.dec	g2178431	957	1107
25	474522.8.dec	2479657H1	884	1058	26	231583.3.dec	210029H1	959	1220
25	474522.8.dec	4862486H1	891	1130	26	231583.3.dec	g2934558	965	1256
25	474522.8.dec	5017477H1	901	1178	26	231583.3.dec	g1887594	966	1261
25	474522.8.dec	4597109H1	926	1192	26	231583.3.dec	g3085821	988	1263
25	474522.8.dec	6315056H1	930	1471	26	231583.3.dec	g1897746	995	1256
25	474522.8.dec	2756593H1	949	1222	26	231583.3.dec	g2816961	1051	1261
25	474522.8.dec	6022083H1	964	1261	26	231583.3.dec	3867687H1	1057	1263
25	474522.8.dec	5928280H1	1009	1286	26	231583.3.dec	g4997299	1059	1256
25	474522.8.dec	6308430H1	1011	1471	26	231583.3.dec	g4148290	1070	1191
25	474522.8.dec	3190055H1	1012	1362	26	231583.3.dec	g3434343	1085	1349
25	474522.8.dec	3121273H1	1014	1306	26	231583.3.dec	g4453294	1086	1174
25	474522.8.dec	361024H1	1016	1123	26	231583.3.dec	g734216	1089	1354
25	474522.8.dec	539721H1	1029	1240	26	231583.3.dec	g1220041	1154	1261
25	474522.8.dec	6304964H1	1033	1418	26	231583.3.dec	g2742647	1165	1261
25	474522.8.dec	1227119H1	1052	1287	26	231583.3.dec	2605033H1	1170	1261
25	474522.8.dec	3498511H1	1067	1352	26	231583.3.dec	g734313	97	379
25	474522.8.dec	4200646H1	1066	1383	26	231583.3.dec	3400848H1	96	306
25	474522.8.dec	4369401H1	1102	1361	26	231583.3.dec	2967782H1	97	401
25	474522.8.dec	3659596H1	1143	1365	26	231583.3.dec	g1874192	86	540
25	474522.8.dec	6569540H1	458	994	26	231583.3.dec	g1967035	93	558
25	474522.8.dec	6099933H1	471	752	26	231583.3.dec	4979528H1	93	369
25	474522.8.dec	4910822H2	165	434	26	231583.3.dec	1867796H1	94	391
25	474522.8.dec	3433764H1	169	424	26	231583.3.dec	4382333H1	94	353
25	474522.8.dec	2105157H1	189	341	26	231583.3.dec	g2178487	95	586
25	474522.8.dec	5710431H2	189	398	26	231583.3.dec	g1858689	97	489
25	474522.8.dec	2082339H1	195	435	26	231583.3.dec	g2963667	887	1261
25	474522.8.dec	3447905H1	196	433	26	231583.3.dec	453167R6	784	1182
25	474522.8.dec	4637623H1	200	438	26	231583.3.dec	453167R7	784	1106
25	474522.8.dec	4977240H1	222	484	26	231583.3.dec	453167H1	784	1110
25	474522.8.dec	1512480H1	242	431	26	231583.3.dec	g3884631	799	942
25	474522.8.dec	550275H1	255	477	26	231583.3.dec	g3308494	819	1256
25	474522.8.dec	678617H1	301	540	26	231583.3.dec	4777585H1	831	921
25	474522.8.dec	2441444H1	353	561	26	231583.3.dec	g2901343	837	1270
25	474522.8.dec	4701793H1	375	600	26	231583.3.dec	2839060T6	839	1358
25	474522.8.dec	5219121H1	447	687	26	231583.3.dec	453167T7	842	1224
25	474522.8.dec	g2180336	378	799	26	231583.3.dec	g2816574	848	1112
25	474522.8.dec	4545853H1	402	642	26	231583.3.dec	3452837H1	849	899
25	474522.8.dec	4768970H1	403	658	26	231583.3.dec	2698055H1	863	1179
25	474522.8.dec	2277358H1	406	689	26	231583.3.dec	g4988189	867	1264
25	474522.8.dec	3642630H1	163	458	26	231583.3.dec	1740714T6	875	1210
25	474522.8.dec	2497236H1	16	330	26	231583.3.dec	3794634H1	136	418
25	474522.8.dec	5862690H1	23	284	26	231583.3.dec	1420279H1	171	439
25	474522.8.dec	g3785848	60	276	26	231583.3.dec	2967782F6	97	607
25	474522.8.dec	g3144117	60	434	26	231583.3.dec	3296842H1	98	362
25	474522.8.dec	g2809679	60	412	26	231583.3.dec	4551367H1	108	354
25	474522.8.dec	g1691199	60	409	26	231583.3.dec	2608335F6	108	417
25	474522.8.dec	g2183371	60	395	26	231583.3.d c	2608335H1	108	358
25	474522.8.dec	g3870546	60	369	26	231583.3.dec	3617251H1	109	253
25	474522.8.dec	g795882	59	322	26	231583.3.dec	3585168H1	117	304
25	474522.8.dec	g3181844	60	244	26	231583.3.dec	g1637120	114	455
25	474522.8.dec	6383954H1	65	338	26	231583.3.d c	4664167H1	899	1122
25	474522.8.dec	g2880771	66	363	26	231583.3.dec	g4003920	783	1181

Table 2 cont.

26	231583.3.dec	2644845H1	298	545
26	231583.3.d c	6343202H1	497	629
26	231583.3.d c	3480411H1	527	700
26	231583.3.dec	g1558633	538	923
26	231583.3.dec	g1198005	591	735
26	231583.3.dec	3718477H1	621	925
26	231583.3.dec	1740714R6	672	1076
26	231583.3.dec	1740714H1	672	900
26	231583.3.dec	5264374H1	693	945
26	231583.3.dec	3799139H1	694	985
26	231583.3.dec	1944836T6	702	1220
26	231583.3.dec	5183988H1	716	985
26	231583.3.dec	2784085T6	722	1223
26	231583.3.dec	2967782T6	733	1356
26	231583.3.dec	2993057H1	755	1011
26	231583.3.dec	4310330H1	62	257
26	231583.3.dec	3074962H1	78	355
26	231583.3.dec	g1897911	87	535
26	231583.3.dec	g2570924	1	1261
26	231583.3.dec	3209157H1	36	306
26	231583.3.dec	3206034H1	61	312
27	215051.5.dec	606683H1	1576	1827
27	215051.5.dec	g3330058	1585	1975
27	215051.5.dec	g2955828	1586	1971
27	215051.5.dec	916910T1	1592	1929
27	215051.5.dec	917301H1	1592	1889
27	215051.5.dec	g4435760	1592	1971
27	215051.5.dec	g3919504	1594	1971
27	215051.5.dec	1890562T6	1604	1934
27	215051.5.dec	g2881509	1608	1971
27	215051.5.dec	g2243514	1642	1972
27	215051.5.dec	g518838	1645	1971
27	215051.5.dec	g561494	1647	1971
27	215051.5.dec	701948H1	1709	1936
27	215051.5.dec	1210895H1	1709	1953
27	215051.5.dec	506634H1	1718	1957
27	215051.5.dec	408624H1	1718	1977
27	215051.5.dec	961530R1	1721	1971
27	215051.5.dec	961530H1	1721	1971
27	215051.5.dec	961530T6	1721	1932
27	215051.5.dec	g5541333	1725	1971
27	215051.5.dec	g645106	1736	1971
27	215051.5.dec	2408613H1	1742	1957
27	215051.5.dec	g5590726	1763	1971
27	215051.5.dec	4664855H1	1769	1853
27	215051.5.dec	3220755H1	1773	1971
27	215051.5.dec	g4125199	1784	1973
27	215051.5.dec	4184491H1	1833	1972
27	215051.5.dec	5710048H1	1843	1971
27	215051.5.dec	g2432388	1843	1972
27	215051.5.dec	3932528H1	1849	1945
27	215051.5.dec	g4901062	1854	1980
27	215051.5.dec	g1697934	1896	2147
27	215051.5.dec	g2805404	1920	1971
27	215051.5.dec	3521103H1	765	959
27	215051.5.dec	734640H1	765	993
27	215051.5.dec	4329448H1	856	1084
27	215051.5.dec	4329250H1	856	997
27	215051.5.dec	5151583H1	872	1113
27	215051.5.dec	1301667F6	882	1216
27	215051.5.dec	1301667H1	882	1086
27	215051.5.dec	g2077260	890	1097
27	215051.5.dec	2812910H1	916	1110
27	215051.5.dec	2727542H1	924	1144
27	215051.5.dec	3935367H1	949	1233
27	215051.5.dec	6571129H1	961	1406
27	215051.5.dec	1559441H1	962	1170
27	215051.5.dec	5674682H1	977	1245
27	215051.5.dec	1909813F6	982	1566
27	215051.5.dec	1909813H1	982	1219
27	215051.5.dec	4541904H1	986	1251
27	215051.5.dec	5154081H1	1013	1265
27	215051.5.dec	5951978H1	1040	1351
27	215051.5.dec	5947813H1	1040	1309
27	215051.5.dec	g1757881	1045	1298
27	215051.5.dec	4948780H1	1054	1328
27	215051.5.dec	1704449H1	1069	1277
27	215051.5.dec	3449928H1	1082	1178
27	215051.5.dec	2549369H1	1083	1324
27	215051.5.dec	5714690H1	1102	1369
27	215051.5.dec	1855956F6	1105	1660
27	215051.5.dec	1855956H1	1105	1379
27	215051.5.dec	1644551H1	1114	1327
27	215051.5.dec	4461495H1	1138	1285
27	215051.5.dec	6483737H1	1145	1663
27	215051.5.dec	g2218767	1144	1467
27	215051.5.dec	1237358H1	1144	1353
27	215051.5.dec	6348133H1	1166	1389
27	215051.5.dec	5048814H1	1259	1453
27	215051.5.dec	g4891899	1271	1673
27	215051.5.dec	1864511F6	1275	1720
27	215051.5.dec	1864511H1	1275	1542
27	215051.5.dec	4710136H1	1286	1373
27	215051.5.dec	4198162H1	1288	1514
27	215051.5.dec	g2318976	1294	1592
27	215051.5.dec	1868512H1	1301	1575
27	215051.5.dec	1868318H1	1301	1562
27	215051.5.dec	g779052	1304	1612
27	215051.5.dec	853710R1	1323	1874
27	215051.5.dec	853710H1	1325	1518
27	215051.5.dec	1855956T6	1332	1935
27	215051.5.dec	4699841T6	1338	1945
27	215051.5.dec	6514011H1	1351	1646
27	215051.5.dec	3519386H1	1361	1603
27	215051.5.dec	5851089H1	1363	1597
27	215051.5.dec	4165079H1	1373	1647
27	215051.5.dec	1301667T6	1378	1933
27	215051.5.dec	2740792H1	1382	1628
27	215051.5.dec	1487718H1	1386	1677
27	215051.5.dec	1890039T6	1402	1933
27	215051.5.dec	968062H1	1407	1590
27	215051.5.dec	1210132R2	1410	1836
27	215051.5.dec	1210132H1	1411	1546
27	215051.5.dec	1216205H1	1412	1647
27	215051.5.dec	2220053T6	1419	1933
27	215051.5.dec	1890562F6	1426	1820
27	215051.5.dec	1890562H1	1426	1685
27	215051.5.dec	2443839T6	1434	1935
27	215051.5.dec	1909813T6	1436	1933
27	215051.5.dec	1554835T6	1440	1930
27	215051.5.dec	5267952H1	1452	1718
27	215051.5.dec	1864511T6	1477	1937
27	215051.5.dec	2666259H1	1478	1661
27	215051.5.dec	g647230	1480	1771
27	215051.5.dec	1548335H1	1492	1640
27	215051.5.dec	2311914H1	1503	1759
27	215051.5.dec	570615R1	1504	1973
27	215051.5.dec	570615H1	1504	1779
27	215051.5.dec	5484618H2	1512	1724
27	215051.5.dec	g2968010	1511	1971
27	215051.5.dec	g756638	1513	1794
27	215051.5.dec	862460R1	1516	1971
27	215051.5.dec	862460T1	1516	1935
27	215051.5.dec	862759H1	1516	1776
27	215051.5.dec	862460H1	1516	1769
27	215051.5.dec	387840H1	1520	1692

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27	215051.5.dec	g5112194	1520	1979	28	277726.5.dec	3349217H1	168	338
27	215051.5.dec	5205618H1	1529	1639	28	277726.5.dec	525355H1	169	427
27	215051.5.dec	g2705032	1533	1973	28	277726.5.dec	3726118H1	174	461
27	215051.5.dec	g5057302	1536	1971	28	277726.5.dec	3726043H1	174	454
27	215051.5.dec	5401923H1	1537	1782	28	277726.5.dec	g1974900	186	396
27	215051.5.dec	g2805413	1541	1971	28	277726.5.dec	3506561H1	190	504
27	215051.5.dec	g4741110	1548	1973	28	277726.5.dec	3237356H1	190	391
27	215051.5.dec	g3962176	1566	1971	28	277726.5.dec	3340715H1	191	320
27	215051.5.dec	3218687H1	1	269	28	277726.5.dec	6550846H1	211	793
27	215051.5.dec	2985007H1	3	266	28	277726.5.dec	5000422H1	232	492
27	215051.5.dec	3218687F6	1	508	28	277726.5.dec	g2161713	257	467
27	215051.5.dec	686080H1	5	246	28	277726.5.dec	3322068H1	272	543
27	215051.5.dec	3744415H1	11	310	28	277726.5.dec	2119348H1	290	558
27	215051.5.dec	3742892H1	10	248	28	277726.5.dec	2663816H1	290	539
27	215051.5.dec	2443839F6	27	475	28	277726.5.dec	3691573H1	301	583
27	215051.5.dec	2443839H1	27	239	28	277726.5.dec	1856677H1	305	577
27	215051.5.dec	3333490H1	33	291	28	277726.5.dec	5573312H1	391	640
27	215051.5.dec	1554835H1	54	250	28	277726.5.dec	260527H1	420	678
27	215051.5.dec	2137635H1	53	261	28	277726.5.dec	260527R6	420	928
27	215051.5.dec	1554835F6	54	534	28	277726.5.dec	3551771H1	436	731
27	215051.5.dec	3333365H1	55	317	28	277726.5.dec	3138453H1	488	778
27	215051.5.dec	4346748H1	139	305	28	277726.5.dec	2941152H1	493	773
27	215051.5.dec	4640737H1	163	441	28	277726.5.dec	g574777	529	777
27	215051.5.dec	3418631H1	272	425	28	277726.5.dec	3271387H1	571	818
27	215051.5.dec	4103113H1	275	556	28	277726.5.dec	623556H1	586	826
27	215051.5.dec	3529273H1	387	659	28	277726.5.dec	4902769H1	626	899
27	215051.5.dec	1428015H1	475	675	28	277726.5.dec	2265514H1	653	897
27	215051.5.dec	g2020323	491	855	28	277726.5.dec	5404966H1	659	921
27	215051.5.dec	1890039F6	492	1001	28	277726.5.dec	5676873H1	664	862
27	215051.5.dec	1890039H1	492	765	28	277726.5.dec	3620380H1	668	927
27	215051.5.dec	1888814H1	492	751	28	277726.5.dec	4574641H1	678	953
27	215051.5.dec	3935045H1	498	778	28	277726.5.dec	1443082F6	680	1209
27	215051.5.dec	2507556H1	508	757	28	277726.5.dec	1443082H1	680	971
27	215051.5.dec	4998065H1	527	816	28	277726.5.dec	4091518H1	690	966
27	215051.5.dec	4890811H1	546	830	28	277726.5.dec	4091719H1	689	801
27	215051.5.dec	4889625H1	546	834	28	277726.5.dec	1302950H1	694	823
27	215051.5.dec	4789725H1	564	765	28	277726.5.dec	4348931H1	702	965
27	215051.5.dec	6483741H1	601	1153	28	277726.5.dec	g2883339	708	1200
27	215051.5.dec	751216H1	629	845	28	277726.5.dec	1342352H1	716	927
27	215051.5.dec	1370005H1	665	913	28	277726.5.dec	2190179H1	722	993
27	215051.5.dec	2220053F6	675	1131	28	277726.5.dec	g1186242	724	1005
27	215051.5.dec	2220053H1	675	922	28	277726.5.dec	2854971H1	748	1007
27	215051.5.dec	4413488H1	704	960	28	277726.5.dec	4588632H1	749	995
27	215051.5.dec	3239878H1	720	965	28	277726.5.dec	4043229H1	778	908
28	277726.5.dec	g2186495	1	366	28	277726.5.dec	1288222H1	781	1021
28	277726.5.dec	149323H1	1	222	28	277726.5.dec	5074476H1	797	1048
28	277726.5.dec	2490760H1	43	248	28	277726.5.dec	6112094H1	829	1081
28	277726.5.dec	593214H1	116	286	28	277726.5.dec	g570683	829	1146
28	277726.5.dec	g884003	124	522	28	277726.5.dec	1493174H1	833	1070
28	277726.5.dec	g776275	126	396	28	277726.5.dec	3520394H1	843	1093
28	277726.5.dec	6421082H1	132	665	28	277726.5.dec	2076038H1	868	1113
28	277726.5.dec	2548048H1	132	378	28	277726.5.dec	5373295H1	872	1062
28	277726.5.dec	653128H1	133	382	28	277726.5.dec	g791313	873	1144
28	277726.5.dec	4648641H1	138	418	28	277726.5.dec	g2219744	899	976
28	277726.5.dec	3695010H1	139	424	28	277726.5.dec	3322247H1	907	1173
28	277726.5.dec	4384281H1	142	399	28	277726.5.dec	1494567H1	912	1144
28	277726.5.dec	6172392H1	143	419	28	277726.5.dec	g1141952	923	1274
28	277726.5.dec	3317093H1	144	410	28	277726.5.dec	612082H1	942	1175
28	277726.5.dec	6134663H1	145	414	28	277726.5.dec	4904840F6	956	1187
28	277726.5.dec	2292124H1	146	371	28	277726.5.dec	4904740H1	958	1172
28	277726.5.dec	4105061H1	150	422	28	277726.5.dec	3466368H1	968	1225
28	277726.5.dec	1313441H1	150	396	28	277726.5.dec	447794H1	1051	1274
28	277726.5.dec	3293982H1	150	393	28	277726.5.dec	453683H1	1052	1206
28	277726.5.dec	3740575F6	157	613	28	277726.5.dec	3865781H1	1079	1447
28	277726.5.dec	2748094H1	158	384	28	277726.5.dec	g1637299	1093	1374
28	277726.5.dec	3740575H1	159	443	28	277726.5.dec	4338458H1	1132	1228
28	277726.5.d c	1996357H1	167	442	29	978637.1.dec	483862R1	1	564
28	277726.5.dec	1996357R6	168	377	29	978637.1.dec	483862R6	1	368

Table 2 cont.

29	978637.1.dec	483862H1	1	197
29	978637.1.dec	2864919H1	1	300
29	978637.1.dec	2693186H1	16	250
29	978637.1.dec	2434044H1	24	230
29	978637.1.dec	268938H1	33	104
29	978637.1.dec	492316H1	35	264
29	978637.1.dec	485739H1	50	172
29	978637.1.dec	g4301223	81	392
29	978637.1.dec	5622671H1	131	371
29	978637.1.dec	2507216H1	144	387
29	978637.1.dec	6264736H1	233	650
29	978637.1.dec	071695H1	257	393
29	978637.1.dec	g1748167	300	662
30	240518.12.dec	3082416H1	363	665
30	240518.12.dec	6410191H1	189	708
30	240518.12.dec	2495029H1	265	585
30	240518.12.dec	2615730H1	266	531
30	240518.12.dec	5086273H1	294	540
30	240518.12.dec	6516585H1	1	268
30	240518.12.dec	2793780H1	6	180
30	240518.12.dec	2793780F6	10	332
30	240518.12.dec	5192419H1	10	174
30	240518.12.dec	4384313H1	622	805
30	240518.12.dec	1257843H1	625	872
30	240518.12.dec	6213295H1	640	922
30	240518.12.dec	6213355H1	640	727
30	240518.12.dec	2793780T6	686	1173
30	240518.12.dec	4346945H1	698	945
30	240518.12.dec	1603893H1	750	951
30	240518.12.dec	4383368H1	780	957
30	240518.12.dec	6076841H1	410	705
30	240518.12.dec	6408502H1	419	1012
30	240518.12.dec	2324406H1	431	705
30	240518.12.dec	6158981H1	459	690
30	240518.12.dec	4575684H1	510	780
30	240518.12.dec	4550371T1	594	1131
30	240518.12.dec	2748726H1	598	840
30	240518.12.dec	2369731H1	537	767
30	240518.12.dec	1811008H1	557	816
30	240518.12.dec	2423235H1	585	808
30	240518.12.dec	1367447H1	560	783
31	413231.8.dec	g771103	1	322
31	413231.8.dec	6478368H1	1	436
31	413231.8.dec	g1378948	4	170
31	413231.8.dec	6597249H1	110	647
31	413231.8.dec	5794471H1	2537	2836
31	413231.8.dec	5784079H1	2537	2808
31	413231.8.dec	5789054H1	2537	2801
31	413231.8.dec	878831R1	1834	2385
31	413231.8.dec	878831H1	1834	2081
31	413231.8.dec	5886741H1	1836	2068
31	413231.8.dec	5883403H1	1835	2065
31	413231.8.dec	5885270H1	1835	2028
31	413231.8.dec	g2001307	1899	2219
31	413231.8.dec	990688H1	1924	2225
31	413231.8.dec	6538992H1	1965	2556
31	413231.8.dec	g1024057	1997	2356
31	413231.8.dec	g2006123	2041	2484
31	413231.8.dec	g2205515	2099	2503
31	413231.8.dec	879803H1	2122	2345
31	413231.8.dec	1613405H1	2122	2324
31	413231.8.dec	1613405F6	2122	2561
31	413231.8.dec	5328147H1	2158	2405
31	413231.8.dec	5330251H1	2158	2427
31	413231.8.dec	2285744H1	2218	2429
31	413231.8.dec	2154518H1	2226	2510
31	413231.8.dec	2271165H1	2305	2571
31	413231.8.dec	5685512H1	2323	2606
31	413231.8.dec	4596295H1	2436	2689
31	413231.8.dec	g3872548	2478	2926
31	413231.8.dec	g4329251	2483	2932
31	413231.8.dec	853069H1	2510	2744
31	413231.8.dec	853069T1	2510	2892
31	413231.8.dec	g2205939	2512	2926
31	413231.8.dec	2202369T6	2515	2890
31	413231.8.dec	g1472416	1131	1342
31	413231.8.dec	617734H1	1136	1399
31	413231.8.dec	g4268510	1145	1424
31	413231.8.dec	g1023192	1154	1464
31	413231.8.dec	g1023206	1154	1432
31	413231.8.dec	g3279813	1180	1426
31	413231.8.dec	151118H1	1197	1424
31	413231.8.dec	g765788	1301	1614
31	413231.8.dec	5385354H1	1349	1618
31	413231.8.dec	5901886H1	1374	1661
31	413231.8.dec	3695547H1	1376	1645
31	413231.8.dec	g817350	1397	1749
31	413231.8.dec	4865292H1	1432	1705
31	413231.8.dec	3244978H1	1445	1685
31	413231.8.dec	2202369F6	1465	1908
31	413231.8.dec	2202369H1	1465	1728
31	413231.8.dec	g4392149	1493	1894
31	413231.8.dec	g884549	1552	1858
31	413231.8.dec	6261831H2	1593	1894
31	413231.8.dec	3932979H1	1713	2006
31	413231.8.dec	3256067H1	1780	2020
31	413231.8.dec	g1404342	625	1095
31	413231.8.dec	g1472473	625	1040
31	413231.8.dec	3440642H2	764	1077
31	413231.8.dec	g923488	768	1139
31	413231.8.dec	5348065H1	808	1062
31	413231.8.dec	2778338H1	875	1099
31	413231.8.dec	2061766T6	881	1382
31	413231.8.dec	151118T6	902	1384
31	413231.8.dec	763265H1	905	1135
31	413231.8.dec	346399H1	921	1114
31	413231.8.dec	346515H1	921	1138
31	413231.8.dec	346515R6	921	1340
31	413231.8.dec	2246263H1	948	1216
31	413231.8.dec	g3889095	965	1424
31	413231.8.dec	g4969522	968	1423
31	413231.8.dec	4783029H1	967	1226
31	413231.8.dec	151118R6	966	1424
31	413231.8.dec	5666039H1	996	1226
31	413231.8.dec	g3644279	1004	1424
31	413231.8.dec	g4080222	1034	1426
31	413231.8.dec	2061850T6	1035	1380
31	413231.8.dec	g3836212	1046	1429
31	413231.8.dec	g1404236	1058	1432
31	413231.8.dec	1321333T6	1069	1375
31	413231.8.dec	g4087402	1072	1426
31	413231.8.dec	1321340H1	1076	1328
31	413231.8.dec	1321333F6	1076	1424
31	413231.8.dec	3039505H1	1083	1346
31	413231.8.dec	g1149424	1090	1424
31	413231.8.dec	6597349H1	110	637
31	413231.8.dec	3974458H1	146	406
31	413231.8.dec	3615019H1	327	624
31	413231.8.dec	5101007H1	328	572
31	413231.8.dec	2728285H1	335	582
31	413231.8.dec	983374H1	355	641
31	413231.8.dec	6368807H1	362	627
31	413231.8.dec	4622254H1	370	555
31	413231.8.dec	2382180H1	373	637
31	413231.8.dec	2061273H1	378	638
31	413231.8.dec	2308479H1	379	647

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31	413231.8.dec	3769001H1	406	676	32	334406.5.dec	g1152031	1317	1544
31	413231.8.dec	2941773H1	409	624	32	334406.5.dec	g883070	1324	1544
31	413231.8.dec	3623712H1	433	645	32	334406.5.dec	g2726848	1336	1479
31	413231.8.dec	2445580T6	449	602	32	334406.5.dec	g4852729	1345	1549
31	413231.8.dec	4150237H1	557	843	32	334406.5.dec	4003449R6	1360	1547
31	413231.8.dec	4150388H1	557	824	32	334406.5.dec	4003449T6	1360	1511
31	413231.8.dec	744151H1	564	646	32	334406.5.dec	g2657484	1360	1549
31	413231.8.dec	1921046H1	565	645	32	334406.5.dec	2374705H1	165	395
31	413231.8.dec	g1023155	2670	2908	32	334406.5.dec	g768949	169	465
31	413231.8.dec	g1114310	2679	2908	32	334406.5.dec	g1200975	170	531
31	413231.8.dec	2672479T6	2704	2886	32	334406.5.dec	1521761H1	168	364
31	413231.8.dec	2672382H1	2711	2926	32	334406.5.dec	2211578H1	168	347
31	413231.8.dec	g923399	2659	2905	32	334406.5.dec	5581563H1	160	401
31	413231.8.dec	2672479F6	2711	2926	32	334406.5.dec	4129984H2	161	384
31	413231.8.dec	2672479H1	2711	2926	32	334406.5.dec	3155206H1	164	456
31	413231.8.dec	g797221	2731	2950	32	334406.5.dec	g676907	166	403
31	413231.8.dec	g797222	2735	2950	32	334406.5.dec	2304981H1	673	830
31	413231.8.dec	2255141H1	2762	2926	32	334406.5.dec	4886618H1	743	1022
31	413231.8.dec	g4891321	2784	2928	32	334406.5.dec	4000520H1	742	992
31	413231.8.dec	320143H1	2804	2927	32	334406.5.dec	4901780H1	558	703
31	413231.8.dec	600957H1	2812	2926	32	334406.5.dec	6098386H1	568	834
31	413231.8.dec	5314446H1	2819	2920	32	334406.5.dec	753486H1	547	749
31	413231.8.dec	5734717H1	2658	2926	32	334406.5.dec	379972H1	550	642
31	413231.8.dec	g1081087	2669	2914	32	334406.5.dec	3648742H1	160	442
31	413231.8.dec	g5664541	2540	2929	32	334406.5.dec	3533417H1	161	441
31	413231.8.dec	g3134725	2555	2929	32	334406.5.dec	4056278H1	153	317
31	413231.8.dec	2293772H1	2571	2808	32	334406.5.dec	2774774H1	154	402
31	413231.8.dec	1833838H1	2607	2866	32	334406.5.dec	1987376H1	154	303
31	413231.8.dec	935396T1	2608	2888	32	334406.5.dec	2663526H1	154	393
31	413231.8.dec	935396R1	2608	2926	32	334406.5.dec	3152813H1	149	443
31	413231.8.dec	935396H1	2608	2917	32	334406.5.dec	2255978H1	149	409
31	413231.8.dec	g1087163	2650	2917	32	334406.5.dec	598721H1	149	383
32	334406.5.dec	g5362949	1134	1552	32	334406.5.dec	g768934	150	474
32	334406.5.dec	g2942255	1145	1553	32	334406.5.dec	3724069H1	150	430
32	334406.5.dec	g4113559	1151	1546	32	334406.5.dec	3421567H1	144	404
32	334406.5.dec	g3180511	1161	1548	32	334406.5.dec	g883178	147	467
32	334406.5.dec	1459707H1	592	811	32	334406.5.dec	g766278	150	467
32	334406.5.dec	1337540H1	598	827	32	334406.5.dec	3670589H1	148	425
32	334406.5.dec	1549787H1	607	813	32	334406.5.dec	4000520T6	1045	1505
32	334406.5.dec	2753112H1	1109	1361	32	334406.5.dec	6191125H1	1060	1370
32	334406.5.dec	6208411H1	1124	1443	32	334406.5.dec	3714591H1	1064	1343
32	334406.5.dec	598722F1	1132	1544	32	334406.5.dec	1393845T6	1029	1508
32	334406.5.dec	3053795H1	134	419	32	334406.5.dec	4772652H1	1067	1326
32	334406.5.dec	3591189H1	135	443	32	334406.5.dec	4702316H1	1086	1358
32	334406.5.dec	1893755H1	136	389	32	334406.5.dec	2500626T6	1090	1520
32	334406.5.dec	3799753H1	141	428	32	334406.5.dec	4655110H1	284	521
32	334406.5.dec	805778H1	141	368	32	334406.5.dec	4537640H1	426	684
32	334406.5.dec	1892092H1	141	323	32	334406.5.dec	1393845F6	521	979
32	334406.5.dec	g1986158	143	402	32	334406.5.dec	1393845H1	521	783
32	334406.5.dec	4003449H1	1360	1484	32	334406.5.dec	3354480H1	529	792
32	334406.5.dec	g567488	1371	1544	32	334406.5.dec	853554H1	535	786
32	334406.5.dec	1459707R1	1172	1548	32	334406.5.dec	2753112R6	1109	1550
32	334406.5.dec	870603H1	1176	1342	32	334406.5.dec	3797885H1	175	352
32	334406.5.dec	g2280242	1186	1545	32	334406.5.dec	5843279H1	176	424
32	334406.5.dec	3793766F6	1187	1544	32	334406.5.dec	2059637R6	180	603
32	334406.5.dec	3793766T6	1188	1498	32	334406.5.dec	2059637H1	180	418
32	334406.5.dec	3793766H1	1187	1469	32	334406.5.dec	3389622H1	130	335
32	334406.5.dec	g2254150	1383	1544	32	334406.5.dec	1527228H1	124	326
32	334406.5.dec	3166948H1	1411	1544	32	334406.5.dec	3580066H1	124	354
32	334406.5.dec	g3432051	1193	1544	32	334406.5.dec	3356208H1	133	378
32	334406.5.dec	g821091	1426	1562	32	334406.5.dec	2846974H1	133	404
32	334406.5.dec	g2817939	1201	1549	32	334406.5.dec	489257H1	1	253
32	334406.5.dec	208122H1	1203	1442	32	334406.5.dec	4153990H1	873	1129
32	334406.5.dec	6213411H1	1238	1521	32	334406.5.dec	4000520R6	742	1199
32	334406.5.dec	g5633621	1255	1546	32	334406.5.dec	3437443H1	880	1113
32	334406.5.dec	g3923801	1299	1550	32	334406.5.dec	2600531F6	902	1274
32	334406.5.dec	g823850	1303	1553	32	334406.5.d c	2600531H1	902	1163
32	334406.5.dec	g4333183	1303	1546	32	334406.5.dec	2513231H1	758	898

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32	334406.5.dec	2600531T6	920	1504
32	334406.5.dec	1537793H1	939	1147
32	334406.5.dec	3934730H1	760	1046
32	334406.5.dec	3930521H1	759	1035
32	334406.5.dec	1993838T6	961	1506
32	334406.5.dec	1993838F6	975	1480
32	334406.5.dec	1993838H1	975	1179
32	334406.5.dec	6567592H1	986	1515
32	334406.5.dec	1682119H1	1009	1189
32	334406.5.dec	2753112T6	1109	1505
32	334406.5.dec	3918341H1	179	482
32	334406.5.dec	5016927H1	190	411
32	334406.5.dec	3328469H1	190	468
32	334406.5.dec	879416H1	160	388
32	334406.5.dec	4159772H1	160	396
32	334406.5.dec	2230254H1	160	418
32	334406.5.dec	2774782H1	154	394
32	334406.5.dec	3271675H1	157	402
32	334406.5.dec	2500626H1	122	339
32	334406.5.dec	2500626F6	122	551
32	334406.5.dec	1527040H1	124	328
33	411429.8.dec	5897635H1	1294	1592
33	411429.8.dec	2107233T6	1445	1989
33	411429.8.dec	871885H1	1449	1604
33	411429.8.dec	2107233R6	1452	1942
33	411429.8.dec	2107233H1	1452	1708
33	411429.8.dec	4935576H1	1154	1419
33	411429.8.dec	2295977H1	1239	1493
33	411429.8.dec	g565995	1538	1879
33	411429.8.dec	1860330T6	1725	1994
33	411429.8.dec	3727538H1	1759	2035
33	411429.8.dec	6195273H1	1828	2124
33	411429.8.dec	4981402H1	2013	2256
33	411429.8.dec	4981202H1	2032	2278
33	411429.8.dec	2731111H1	2032	2266
33	411429.8.dec	3216854H1	66	250
33	411429.8.dec	g1774637	66	230
33	411429.8.dec	g2505764	163	553
33	411429.8.dec	g2505717	164	553
33	411429.8.dec	g2354084	169	553
33	411429.8.dec	g3597881	170	553
33	411429.8.dec	983855H1	171	439
33	411429.8.dec	983855T1	171	507
33	411429.8.dec	g2350558	172	519
33	411429.8.dec	g3922578	174	554
33	411429.8.dec	g3804796	197	530
33	411429.8.dec	g3700866	195	558
33	411429.8.dec	g2958062	197	554
33	411429.8.dec	g4762322	200	553
33	411429.8.dec	1433691H1	205	437
33	411429.8.dec	4750950H1	206	447
33	411429.8.dec	3818447H1	207	471
33	411429.8.dec	g3145205	216	553
33	411429.8.dec	214471H1	180	379
33	411429.8.dec	g1773451	188	558
33	411429.8.dec	g3739713	194	564
33	411429.8.dec	3269162H1	35	293
33	411429.8.dec	583445H1	36	292
33	411429.8.dec	583800H1	38	289
33	411429.8.dec	g1390456	34	309
33	411429.8.dec	3143351H1	36	377
33	411429.8.dec	6369627H1	35	374
33	411429.8.dec	g2397550	216	554
33	411429.8.dec	4983757H1	231	497
33	411429.8.dec	3900386H1	241	512
33	411429.8.dec	g2985846	247	564
33	411429.8.dec	4500345H1	249	513
33	411429.8.dec	4500394H1	249	503
33	411429.8.dec	g5630906	250	562
33	411429.8.dec	g3733942	250	553
33	411429.8.dec	1425369H1	268	511
33	411429.8.dec	g2276646	268	554
33	411429.8.dec	g2727285	269	530
33	411429.8.dec	g771032	295	550
33	411429.8.dec	g2236485	301	567
33	411429.8.dec	g3191279	306	562
33	411429.8.dec	g2355216	306	553
33	411429.8.dec	522986H1	309	553
33	411429.8.dec	g2155125	319	556
33	411429.8.dec	620342H1	323	563
33	411429.8.dec	055557H1	324	512
33	411429.8.dec	233885H1	327	553
33	411429.8.dec	g3070619	338	553
33	411429.8.dec	1495696H1	347	553
33	411429.8.dec	g1390675	348	617
33	411429.8.dec	g1615202	388	764
33	411429.8.dec	2729807H1	391	553
33	411429.8.dec	2255134H1	391	553
33	411429.8.dec	g1101419	396	623
33	411429.8.dec	g570590	407	702
33	411429.8.dec	g3434666	419	564
33	411429.8.dec	g4283227	426	553
33	411429.8.dec	208960H1	446	553
33	411429.8.dec	2933205H2	469	527
33	411429.8.dec	4592438H1	488	557
33	411429.8.dec	1860330F6	498	971
33	411429.8.dec	1860330H1	498	705
33	411429.8.dec	839111H1	519	577
33	411429.8.dec	4517563H1	602	839
33	411429.8.dec	459076H1	878	1070
33	411429.8.dec	4436715H1	973	1254
33	411429.8.dec	052139H1	1037	1257
33	411429.8.dec	2756951H1	73	320
33	411429.8.dec	2746334H1	72	304
33	411429.8.dec	4344936H1	75	357
33	411429.8.dec	3369795H1	75	391
33	411429.8.dec	6106562H1	76	391
33	411429.8.dec	2742002H1	76	321
33	411429.8.dec	616088H1	76	307
33	411429.8.dec	3623928H1	78	253
33	411429.8.dec	4047691H1	72	360
33	411429.8.dec	660714H1	72	340
33	411429.8.dec	1544763H1	72	156
33	411429.8.dec	1544763T1	72	515
33	411429.8.dec	4801283H1	72	316
33	411429.8.dec	4434543H1	72	342
33	411429.8.dec	828360H1	72	227
33	411429.8.dec	1424886T6	72	500
33	411429.8.dec	4566537H1	72	324
33	411429.8.dec	1424886R1	72	467
33	411429.8.dec	2945025H1	72	348
33	411429.8.dec	4202491H1	72	335
33	411429.8.dec	3900464H1	72	339
33	411429.8.dec	4045408H1	1	108
33	411429.8.dec	1730041H1	1	231
33	411429.8.dec	1730041F6	1	423
33	411429.8.dec	3449059H1	8	206
33	411429.8.dec	1870524H1	72	332
33	411429.8.dec	1424886H1	72	304
33	411429.8.dec	5945503H1	72	365
33	411429.8.dec	4001455H1	72	346
33	411429.8.dec	2728288H1	72	316
33	411429.8.dec	3832210H1	72	363
33	411429.8.dec	1322007H1	72	304
33	411429.8.d c	2270423H1	72	359
33	411429.8.dec	524972H1	73	313

Table 2 cont.

33	411429.8.dec	2458668H1	72	310	33	411429.8.dec	1533126H1	81	293
33	411429.8.dec	2318662H1	73	318	33	411429.8.dec	6569517H1	81	554
33	411429.8.dec	4727411H1	38	306	33	411429.8.dec	g2563779	81	553
33	411429.8.dec	g2027446	37	341	33	411429.8.dec	4702460H1	83	319
33	411429.8.dec	6171692H1	36	321	33	411429.8.dec	1730041T6	82	573
33	411429.8.dec	3235720H1	38	288	33	411429.8.dec	345191H1	83	342
33	411429.8.dec	g1199085	8	310	33	411429.8.dec	4702560H1	83	290
33	411429.8.dec	5015140H1	22	268	33	411429.8.dec	2838501H1	84	308
33	411429.8.dec	4973236H1	23	287	33	411429.8.dec	4803067H1	84	364
33	411429.8.dec	3504918H1	23	331	33	411429.8.dec	4643023H1	31	280
33	411429.8.dec	2732793H1	23	261	33	411429.8.dec	g614422	28	421
33	411429.8.dec	5307596H1	23	208	33	411429.8.dec	g571075	31	320
33	411429.8.dec	2290053H1	23	283	33	411429.8.dec	2859927H1	33	121
33	411429.8.dec	935261H1	23	344	33	411429.8.dec	4758554H1	35	136
33	411429.8.dec	4642206H1	23	280	33	411429.8.dec	4607294H1	35	295
33	411429.8.dec	6425381H1	24	557	33	411429.8.dec	g1471975	34	265
33	411429.8.dec	6421382H1	24	487	33	411429.8.dec	4158078H1	35	132
33	411429.8.dec	935261R1	23	552	33	411429.8.dec	1459333H1	35	271
33	411429.8.dec	6551068H1	24	519	33	411429.8.dec	5043453H1	38	181
33	411429.8.dec	5301771H1	24	271	34	320674.7.dec	2526141H1	34	277
33	411429.8.dec	6152039H1	24	306	34	320674.7.dec	3993581H1	34	297
33	411429.8.dec	g1961004	29	437	34	320674.7.dec	3855165H1	34	310
33	411429.8.dec	g2616218	36	550	34	320674.7.dec	2483305H1	33	111
33	411429.8.dec	3168144H1	40	315	34	320674.7.dec	3598427H1	33	333
33	411429.8.dec	5988537H1	45	331	34	320674.7.dec	2262351H1	33	285
33	411429.8.dec	5277041H1	45	194	34	320674.7.dec	4906077H2	34	291
33	411429.8.dec	2392910H1	47	286	34	320674.7.dec	2961950H1	33	341
33	411429.8.dec	2389359H1	47	269	34	320674.7.dec	3465890H1	46	258
33	411429.8.dec	1495932H1	47	254	34	320674.7.dec	3465439H1	46	267
33	411429.8.dec	3350404H1	50	305	34	320674.7.dec	5216182H1	46	272
33	411429.8.dec	6013184H1	52	319	34	320674.7.dec	1243437H1	46	314
33	411429.8.dec	g1349657	53	531	34	320674.7.dec	g1506757	990	1130
33	411429.8.dec	g1928545	53	475	34	320674.7.dec	3508843H1	1002	1277
33	411429.8.dec	5667759H1	60	268	34	320674.7.dec	1829807F6	914	1431
33	411429.8.dec	1459333R1	121	563	34	320674.7.dec	750246H1	971	1179
33	411429.8.dec	026090H1	124	305	34	320674.7.dec	6312943H1	1058	1591
33	411429.8.dec	026100H1	124	211	34	320674.7.dec	g2030862	1114	1425
33	411429.8.dec	2379813H1	124	340	34	320674.7.dec	3968678H1	1273	1462
33	411429.8.dec	g2278874	122	553	34	320674.7.dec	2550116H1	1443	1710
33	411429.8.dec	2671459H1	124	371	34	320674.7.dec	4542257H1	1543	1813
33	411429.8.dec	3120237H1	124	382	34	320674.7.dec	2260015H1	1623	1880
33	411429.8.dec	1359149H1	124	358	34	320674.7.dec	1829807T6	1682	2173
33	411429.8.dec	g4005985	126	561	34	320674.7.dec	6422539H1	1687	2025
33	411429.8.dec	g2905071	147	553	34	320674.7.dec	3246823T6	1797	2178
33	411429.8.dec	g3070620	155	553	34	320674.7.dec	3246823H1	1803	2050
33	411429.8.dec	6605957H1	158	553	34	320674.7.dec	3246823F6	1803	2215
33	411429.8.dec	5482372H1	85	346	34	320674.7.dec	g4985323	1823	2215
33	411429.8.dec	g3870143	86	555	34	320674.7.dec	g1506758	1889	2215
33	411429.8.dec	g616292	90	404	34	320674.7.dec	g653132	1935	2217
33	411429.8.dec	g2789293	89	553	34	320674.7.dec	2192404H1	33	283
33	411429.8.dec	g616059	89	482	34	320674.7.dec	4406455H1	35	112
33	411429.8.dec	g616060	89	488	34	320674.7.dec	792516R1	34	615
33	411429.8.dec	1490450H1	93	296	34	320674.7.dec	982261H1	54	379
33	411429.8.dec	4796417H1	92	213	34	320674.7.dec	g1983177	54	245
33	411429.8.dec	g1615201	94	505	34	320674.7.dec	3592179H1	55	361
33	411429.8.dec	2113476H1	95	364	34	320674.7.dec	265449H1	54	194
33	411429.8.dec	5573421H1	97	344	34	320674.7.dec	3839116H1	56	357
33	411429.8.dec	g3870977	103	553	34	320674.7.dec	746643R1	54	488
33	411429.8.dec	g1969196	104	553	34	320674.7.dec	4241528H1	56	417
33	411429.8.dec	g1954732	107	408	34	320674.7.dec	g1364521	357	615
33	411429.8.dec	3694471H1	106	348	34	320674.7.dec	g646510	373	615
33	411429.8.dec	1907926T6	109	515	34	320674.7.d c	g3840775	383	615
33	411429.8.dec	g1635916	112	224	34	320674.7.d c	g3743793	384	615
33	411429.8.dec	1907926H1	116	370	34	320674.7.dec	g5437001	393	615
33	411429.8.dec	1907926F6	116	553	34	320674.7.dec	2207163H1	395	662
33	411429.8.dec	546808H1	77	369	34	320674.7.dec	g2985510	508	590
33	411429.8.dec	g2616182	77	556	34	320674.7.dec	g4074428	518	615
33	411429.8.dec	g3093055	77	557	34	320674.7.dec	g3737713	519	615

Table 2 cont.

34	320674.7.d c	g2963534	575	678
34	320674.7.d c	g3597109	583	671
34	320674.7.dec	1382266H1	333	577
34	320674.7.dec	1397144H1	333	596
34	320674.7.dec	g3738995	340	622
34	320674.7.d c	g1766491	351	588
34	320674.7.dec	g2563628	184	518
34	320674.7.dec	g2360343	251	614
34	320674.7.dec	g587198	254	615
34	320674.7.dec	g2821179	255	620
34	320674.7.dec	g3280980	185	620
34	320674.7.dec	g3753821	241	622
34	320674.7.dec	g1933057	242	615
34	320674.7.dec	4914556T8	244	573
34	320674.7.dec	2324436H1	248	510
34	320674.7.dec	2323128H1	248	506
34	320674.7.dec	g1898237	260	615
34	320674.7.dec	1910935H1	261	501
34	320674.7.dec	g2195148	262	620
34	320674.7.dec	4358201H1	48	330
34	320674.7.dec	3391767H1	49	330
34	320674.7.dec	g1795515	53	403
34	320674.7.dec	5345961H1	52	290
34	320674.7.dec	1748443H1	52	184
34	320674.7.dec	5162936H1	860	952
34	320674.7.dec	2205827F6	776	1153
34	320674.7.dec	g1993176	789	1083
34	320674.7.dec	g766921	793	1016
34	320674.7.dec	2479851H1	863	1088
34	320674.7.dec	4746673H1	26	257
34	320674.7.dec	4848226H1	26	270
34	320674.7.dec	4436505H1	27	291
34	320674.7.dec	2097725R6	25	417
34	320674.7.dec	2897132H1	25	216
34	320674.7.dec	5118730H1	29	313
34	320674.7.dec	g2001453	73	380
34	320674.7.dec	5670374H1	74	191
34	320674.7.dec	1442776H1	75	321
34	320674.7.dec	4018073H1	108	192
34	320674.7.dec	1346531H1	125	362
34	320674.7.dec	1943883R6	139	612
34	320674.7.dec	1943883H1	139	389
34	320674.7.dec	3269622H1	143	381
34	320674.7.dec	g4260477	145	617
34	320674.7.dec	g3753672	153	622
34	320674.7.dec	3839247H1	159	450
34	320674.7.dec	g3960404	161	619
34	320674.7.dec	g5038447	182	615
34	320674.7.dec	g4311691	183	615
34	320674.7.dec	2757483H1	262	520
34	320674.7.dec	586727H1	262	507
34	320674.7.dec	g1773968	264	555
34	320674.7.dec	g4186990	265	615
34	320674.7.dec	g2901581	266	615
34	320674.7.dec	2940232H1	274	539
34	320674.7.dec	6168189H1	275	615
34	320674.7.dec	g3962074	278	615
34	320674.7.dec	g2254620	314	615
34	320674.7.dec	2366954H1	39	270
34	320674.7.dec	2470102H1	39	245
34	320674.7.dec	g1281396	42	436
34	320674.7.dec	2850901H1	39	352
34	320674.7.dec	4055419H1	45	162
34	320674.7.dec	5867303H1	39	321
34	320674.7.dec	4110833H1	45	336
34	320674.7.dec	2947054H2	41	327
34	320674.7.dec	4275274H1	45	328
34	320674.7.dec	2522462H1	34	281
34	320674.7.dec	2783335H2	34	278
34	320674.7.dec	792516H1	34	258
34	320674.7.dec	721775H1	34	225
34	320674.7.dec	2534641H1	34	258
34	320674.7.dec	632180H1	34	282
34	320674.7.dec	3520179H1	34	360
34	320674.7.dec	g1775483	37	155
34	320674.7.dec	5033665H1	34	295
34	320674.7.dec	4844745H1	47	272
34	320674.7.dec	2659859H1	47	288
34	320674.7.dec	1922312H1	47	316
34	320674.7.dec	6169157H1	46	136
34	320674.7.dec	6008947H1	62	371
34	320674.7.dec	6508822H1	65	157
34	320674.7.dec	2174565H1	68	198
34	320674.7.dec	2922846H1	68	336
34	320674.7.dec	3739613H1	68	247
34	320674.7.dec	3175571H1	68	321
34	320674.7.dec	1623101H1	46	256
34	320674.7.dec	5289080H1	46	205
34	320674.7.dec	638816H1	46	190
34	320674.7.dec	1894775H1	46	296
34	320674.7.dec	1748326H1	52	289
34	320674.7.dec	5554087H1	52	318
34	320674.7.dec	5167107H2	54	275
34	320674.7.dec	746643H1	54	280
34	320674.7.dec	1705647H1	54	286
34	320674.7.dec	3560375H1	56	335
34	320674.7.dec	3834716H1	57	237
34	320674.7.dec	1972338H1	57	299
34	320674.7.dec	4513638H1	57	294
34	320674.7.dec	5857125H1	58	331
34	320674.7.dec	5856825H1	58	317
34	320674.7.dec	6027442H1	58	353
34	320674.7.dec	6321410H1	59	346
34	320674.7.dec	2815776H1	58	328
34	320674.7.dec	5047756H1	59	308
34	320674.7.dec	1726967H1	60	299
34	320674.7.dec	3292839H1	592	832
34	320674.7.dec	g2616212	614	1129
34	320674.7.dec	4767122H1	642	906
34	320674.7.dec	641657H1	695	955
34	320674.7.dec	g653248	704	1005
34	320674.7.dec	2205827H1	776	1019
34	320674.7.dec	3342350H1	32	293
34	320674.7.dec	3717588H1	32	326
34	320674.7.dec	788535H1	32	141
34	320674.7.dec	g1267659	32	207
34	320674.7.dec	2525163H1	31	271
34	320674.7.dec	5118730F6	29	451
34	320674.7.dec	4973794H1	28	202
34	320674.7.dec	5565672H1	31	273
34	320674.7.dec	5493858H1	31	269
34	320674.7.dec	g2185030	32	361
34	320674.7.dec	2139545H1	31	287
34	320674.7.dec	4975303H1	37	313
34	320674.7.dec	111846R1	38	615
34	320674.7.dec	111846R6	38	525
34	320674.7.dec	3190766H1	38	351
34	320674.7.dec	g1933174	39	461
34	320674.7.dec	3336563H1	39	299
34	320674.7.dec	1340623H1	1	218
34	320674.7.d c	2635990H1	2	250
34	320674.7.dec	5349841H1	12	250
34	320674.7.dec	111846T6	22	593
34	320674.7.dec	2097717H1	25	287
35	197267.1.dec	1473808H1	1	110
35	197267.1.dec	g1548716	7	330

Table 2 cont.

35	197267.1.dec	g1940204	1	464	
35	197267.1.dec	2204071H1	40	222	
35	197267.1.dec	6298845H1	40	208	
35	197267.1.dec	g1859154	40	370	
35	197267.1.dec	4772879H1	348	629	
35	197267.1.dec	319110T6	345	865	
35	197267.1.dec	5028542H1	423	679	
35	197267.1.dec	g2537655	437	871	
35	197267.1.dec	977791H1	357	574	
35	197267.1.dec	4240190H1	359	605	
35	197267.1.dec	2771133H1	361	606	
35	197267.1.dec	977791R1	357	785	
35	197267.1.dec	2132792R6	373	512	
35	197267.1.dec	g3254447	461	913	
35	197267.1.dec	g3961279	466	901	
35	197267.1.dec	1637850H1	450	654	
35	197267.1.dec	1348899H1	438	697	
35	197267.1.dec	1635340H1	450	654	
35	197267.1.dec	g1471157	339	531	
35	197267.1.dec	2413149H1	403	565	
35	197267.1.dec	612807H1	427	521	
35	197267.1.dec	5122537T6	413	870	
35	197267.1.dec	5213230H1	418	644	
35	197267.1.dec	4365757H1	421	681	
35	197267.1.dec	g896705	691	905	
35	197267.1.dec	g3601113	695	908	
35	197267.1.dec	2751946H1	389	648	
35	197267.1.dec	1927601H1	386	626	
35	197267.1.dec	5551489H1	706	900	
35	197267.1.dec	g1855688	706	918	
35	197267.1.dec	g2464352	752	910	
35	197267.1.dec	g1471158	757	906	
35	197267.1.dec	2127070H1	769	901	
35	197267.1.dec	g1114641	695	877	
35	197267.1.dec	611349H1	563	824	
35	197267.1.dec	2491963H1	563	818	
35	197267.1.dec	g3232145	568	912	
35	197267.1.dec	g3802367	572	924	
35	197267.1.dec	g1548831	584	877	
35	197267.1.dec	5164893H1	599	862	
35	197267.1.dec	817768H1	317	568	
35	197267.1.dec	2501178H1	276	513	
35	197267.1.dec	g842912	278	529	
35	197267.1.dec	g920007	323	566	
35	197267.1.dec	2500349T6	331	858	
35	197267.1.dec	1803588T6	396	863	
35	197267.1.dec	g1166133	395	561	
35	197267.1.dec	g5365013	508	913	
35	197267.1.dec	g4005355	504	901	
35	197267.1.dec	5992634H1	507	803	
35	197267.1.dec	1699741H1	374	602	
35	197267.1.dec	1616045H1	378	596	
35	197267.1.dec	g1856065	227	715	
35	197267.1.dec	5313986H1	245	479	
35	197267.1.dec	3984239H1	265	539	
35	197267.1.dec	g810072	267	601	
35	197267.1.dec	g2064405	265	723	
35	197267.1.dec	g3988037	521	919	
35	197267.1.dec	906113H1	541	796	
35	197267.1.dec	906113R1	541	901	
35	197267.1.dec	2132792H1	436	685	
35	197267.1.dec	955324H1	438	680	
35	197267.1.d c	955324R1	438	901	
35	197267.1.d c	1803588H1	72	335	
35	197267.1.d c	1494078H1	66	277	
35	197267.1.dec	2277953H1	119	392	
35	197267.1.dec	2500349H1	126	376	
35	197267.1.dec	4835330H1	453	722	
35	197267.1.dec	1621983H1	453	665	
35	197267.1.dec	4567732H1	489	759	
35	197267.1.dec	374248H1	498	720	
35	197267.1.dec	1473995H1	616	805	
35	197267.1.dec	5986850H1	620	901	
35	197267.1.dec	g4511097	621	901	
35	197267.1.dec	6212219H1	625	901	
35	197267.1.dec	g4332172	627	914	
35	197267.1.dec	2132792T6	636	862	
35	197267.1.dec	3374148H1	269	527	
35	197267.1.dec	g1025985	271	535	
35	197267.1.dec	g896704	276	572	
35	197267.1.dec	2751121H1	551	642	
35	197267.1.dec	319110H1	228	610	
35	197267.1.dec	4651030H1	220	462	
35	197267.1.dec	3246169H1	221	454	
35	197267.1.dec	4856582H1	213	492	
35	197267.1.dec	319110R6	228	742	
35	197267.1.dec	1348978H1	438	680	
35	197267.1.dec	2687592H1	650	886	
35	197267.1.dec	5083760H1	677	931	
35	197267.1.dec	2204071T6	678	858	
35	197267.1.dec	g809963	684	901	
35	197267.1.dec	2103287H1	690	912	
35	197267.1.dec	2872292H1	466	733	
35	197267.1.dec	4958730H1	469	733	
35	197267.1.dec	3267673H1	453	707	
35	197267.1.dec	g5110236	456	914	
35	197267.1.dec	537271H1	542	794	
35	197267.1.dec	905790T1	541	858	
35	197267.1.dec	3986769H1	208	465	
35	197267.1.dec	g2836064	779	901	
35	197267.1.dec	g3665793	787	901	
35	197267.1.dec	g2969091	800	901	
35	197267.1.dec	2500349F6	126	614	
35	197267.1.dec	3886423H1	100	354	
35	197267.1.dec	2604501H1	113	370	
35	197267.1.dec	3899701H1	225	501	
35	197267.1.dec	2717183H1	123	359	
35	197267.1.dec	3614668H1	134	417	
35	197267.1.dec	2500164H1	126	380	
35	197267.1.dec	g3770372	602	901	
35	197267.1.dec	1473995T1	616	861	
36	332335.1.dec	3430852H1	977	1229	
36	332335.1.dec	646350H1	813	1007	
36	332335.1.dec	4556145H1	904	1173	
36	332335.1.dec	3430852F6	977	1428	
36	332335.1.dec	1335220H1	1034	1268	
36	332335.1.dec	4187132H1	1949	2100	
36	332335.1.dec	5870021H1	1993	2225	
36	332335.1.dec	5028581H1	2062	2315	
36	332335.1.dec	g1957941	2073	2387	
36	332335.1.dec	4875910H1	2074	2367	
36	332335.1.dec	3414856H1	2180	2430	
36	332335.1.dec	4896022H1	1994	2275	
36	332335.1.dec	6457742H1	1201	1756	
36	332335.1.dec	g723998	1363	1550	
36	332335.1.dec	1580966F6	1382	1883	
36	332335.1.dec	5864333F6	614	1169	
36	332335.1.dec	5864333H1	614	883	
36	332335.1.dec	3212701H1	1	293	
36	332335.1.dec	6421135H1	202	783	
36	332335.1.dec	3378675H1	388	636	
36	332335.1.dec	g751133	1469	1724	
36	332335.1.dec	4933390H1	1567	1771	
36	332335.1.dec	1805556F6	1676	2167	
36	332335.1.dec	1805556H1	1676	1931	
36	332335.1.dec	3773837H1	1716	1997	

Table 2 cont.

36	332335.1.dec	4766037H1	1849	2127
36	332335.1.dec	5394518H1	1375	1544
36	332335.1.d c	1580966H1	1382	1579
36	332335.1.dec	6115174H1	404	652
36	332335.1.dec	4724178H1	498	754
36	332335.1.dec	3096159H1	1460	1730
36	332335.1.dec	3691429H1	530	749
36	332335.1.dec	g723913	2634	2724
36	332335.1.dec	234119H1	2515	2732
36	332335.1.dec	1843866H1	2588	2698
36	332335.1.dec	g2238687	2504	2724
36	332335.1.dec	1751415H1	2616	2698
36	332335.1.dec	1751415F6	2616	2698
36	332335.1.dec	1751415T6	2628	2698
36	332335.1.dec	3430852T6	2255	2725
36	332335.1.dec	1805556T6	2355	2730
36	332335.1.dec	g751134	2487	2724
37	238992.13.dec	4801804H1	1	270
37	238992.13.dec	g4738297	844	1138
37	238992.13.dec	5325955H1	335	555
37	238992.13.dec	1981188H1	385	566
37	238992.13.dec	g2000913	416	590
37	238992.13.dec	506041H1	454	598
37	238992.13.dec	988252T6	468	1099
37	238992.13.dec	2101260H1	473	725
37	238992.13.dec	4775977H1	487	758
37	238992.13.dec	4132042H1	638	890
37	238992.13.dec	2226878T6	639	1100
37	238992.13.dec	4131950H2	638	892
37	238992.13.dec	5911618H1	619	894
37	238992.13.dec	2262124H1	622	875
37	238992.13.dec	994076H1	626	866
37	238992.13.dec	1811058T6	638	1100
37	238992.13.dec	781943H1	636	917
37	238992.13.dec	2182085H1	158	425
37	238992.13.dec	619594H1	170	427
37	238992.13.dec	5204803H1	191	437
37	238992.13.dec	921438H1	222	499
37	238992.13.dec	6495685H1	233	746
37	238992.13.dec	2465087H1	237	430
37	238992.13.dec	5870435H1	239	527
37	238992.13.dec	4466185H1	263	436
37	238992.13.dec	g3148442	278	680
37	238992.13.dec	1800070H1	335	583
37	238992.13.dec	5266304H1	602	886
37	238992.13.dec	1355072H1	601	853
37	238992.13.dec	1541758H1	601	811
37	238992.13.dec	g2398462	831	1132
37	238992.13.dec	664227H1	838	1109
37	238992.13.dec	g3755478	840	1139
37	238992.13.dec	5223778H1	844	1018
37	238992.13.dec	3143814H1	823	1141
37	238992.13.dec	3143187H1	823	1131
37	238992.13.dec	6343865H1	507	780
37	238992.13.dec	6538146H1	524	1082
37	238992.13.dec	1986206H1	539	801
37	238992.13.dec	5313607H1	539	789
37	238992.13.dec	3270285H1	539	765
37	238992.13.dec	1986206R6	539	910
37	238992.13.dec	767764T6	542	1093
37	238992.13.dec	1637874H1	577	806
37	238992.13.dec	4600931H1	582	880
37	238992.13.dec	1655010T6	580	1174
37	238992.13.dec	g907966	595	794
37	238992.13.dec	4413503T8	718	1104
37	238992.13.dec	4858873H1	698	749
37	238992.13.dec	g5546065	728	1139
37	238992.13.dec	4460527H1	711	865
37	238992.13.dec	5784262H1	760	991
37	238992.13.dec	g3422246	763	1145
37	238992.13.dec	g1851666	49	286
37	238992.13.dec	995559H1	645	937
37	238992.13.dec	1635341H1	734	938
37	238992.13.dec	g4889628	737	1147
37	238992.13.dec	1986206T6	764	1166
37	238992.13.dec	5792569H1	760	1057
37	238992.13.dec	1701703T6	639	1164
37	238992.13.dec	2323432H1	643	897
37	238992.13.dec	782457H1	636	882
37	238992.13.dec	2280328H1	636	902
37	238992.13.dec	2776895H1	637	900
37	238992.13.dec	2129269H1	1053	1132
37	238992.13.dec	560897H1	1075	1138
37	238992.13.dec	5433954H1	1091	1207
37	238992.13.dec	3318824H1	763	1032
37	238992.13.dec	g3753170	765	1147
37	238992.13.dec	g2277454	770	1062
37	238992.13.dec	5429341H1	611	823
37	238992.13.dec	g1193876	610	799
37	238992.13.dec	3643443H1	615	881
37	238992.13.dec	3385332H1	615	880
37	238992.13.dec	2800721H1	617	861
37	238992.13.dec	2951181H1	618	892
37	238992.13.dec	1300928T6	687	1117
37	238992.13.dec	3843689H1	688	958
37	238992.13.dec	g3756865	691	1137
37	238992.13.dec	6107082H1	652	952
37	238992.13.dec	4847550H1	655	885
37	238992.13.dec	5330638T6	668	1109
37	238992.13.dec	g2752175	671	838
37	238992.13.dec	1552390H1	680	873
37	238992.13.dec	2081835T6	683	1184
37	238992.13.dec	5606465H1	682	910
37	238992.13.dec	1473638H1	645	894
37	238992.13.dec	1655911H1	645	843
37	238992.13.dec	1798756T6	506	1098
37	238992.13.dec	506181H1	492	672
37	238992.13.dec	1214029H1	487	706
37	238992.13.dec	4072388H1	844	1098
37	238992.13.dec	5680287H1	866	1104
37	238992.13.dec	4185214H1	870	1205
37	238992.13.dec	817636H1	881	1138
37	238992.13.dec	6102141H1	883	1137
37	238992.13.dec	817636T1	882	1104
37	238992.13.dec	3329194T6	887	1169
37	238992.13.dec	3621515H1	888	1105
37	238992.13.dec	g825072	890	1148
37	238992.13.dec	g678520	890	1138
37	238992.13.dec	3458067H1	891	1138
37	238992.13.dec	g5152342	913	1138
37	238992.13.dec	3409541H1	915	1138
37	238992.13.dec	2569561H1	919	1178
37	238992.13.dec	4368210H1	942	1138
37	238992.13.dec	2357876H1	945	1138
37	238992.13.dec	3729584H1	947	1138
37	238992.13.dec	4509315H1	955	1231
37	238992.13.dec	4542916H1	955	1225
37	238992.13.dec	g706241	965	1138
37	238992.13.dec	788265H1	986	1138
37	238992.13.dec	g2215495	1025	1148
37	238992.13.dec	3159415H1	822	1115
37	238992.13.dec	1349465H1	774	981
37	238992.13.dec	5102865H1	777	1037
37	238992.13.dec	3860037H1	782	1061
37	238992.13.dec	6327352H1	788	1042
37	238992.13.dec	g3092108	795	1137

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38	199736.1.dec	g2903286	274	597	41	481454.4.dec	719870H1	1007	1256
38	199736.1.dec	1522915H1	380	484	41	481454.4.dec	965365R1	1028	1602
38	199736.1.dec	6593543H1	423	940	41	481454.4.dec	965365H1	1028	1348
38	199736.1.dec	2890957H1	669	931	41	481454.4.dec	1422810H1	1031	1281
38	199736.1.dec	g2432628	1	333	41	481454.4.dec	705397H1	166	315
38	199736.1.dec	g1967342	1	450	41	481454.4.dec	081492H1	179	342
38	199736.1.dec	g3751279	1	444	41	481454.4.dec	712266H1	181	277
38	199736.1.dec	1444281H1	1	257	41	481454.4.dec	3442620H1	186	441
38	199736.1.dec	1444281F6	1	505	41	481454.4.dec	724216H1	1720	1958
38	199736.1.dec	g4289858	4	321	41	481454.4.dec	724216R6	1720	2130
38	199736.1.dec	1439532H1	13	297	41	481454.4.dec	551787H1	1737	1894
38	199736.1.dec	1439532F1	13	501	41	481454.4.dec	722578H1	1738	2006
38	199736.1.dec	g2457237	18	476	41	481454.4.dec	1423789H1	1527	1740
38	199736.1.dec	g3043040	18	436	41	481454.4.dec	1385707H1	1538	1767
38	199736.1.dec	3034279H1	58	354	41	481454.4.dec	1388173H1	1538	1785
38	199736.1.dec	3031157H1	58	360	41	481454.4.dec	4356537H1	1542	1660
39	228864.5.dec	943941T1	417	714	41	481454.4.dec	1261250R1	1542	2131
39	228864.5.dec	2240562H1	433	692	41	481454.4.dec	1261250R6	1542	2051
39	228864.5.dec	2569601H1	437	681	41	481454.4.dec	1261250H1	1542	1774
39	228864.5.dec	751050H1	466	691	41	481454.4.dec	4755269H1	1597	1863
39	228864.5.dec	4424104H1	493	743	41	481454.4.dec	3553105H1	1603	1900
39	228864.5.dec	2101758H1	516	757	41	481454.4.dec	3741144H1	1646	1862
39	228864.5.dec	5608727H1	526	747	41	481454.4.dec	698444H1	1650	1893
39	228864.5.dec	137261H1	217	384	41	481454.4.dec	1423073H1	1667	1876
39	228864.5.dec	3469340H1	217	460	41	481454.4.dec	2497753H1	1678	1923
39	228864.5.dec	2438390H1	224	456	41	481454.4.dec	722589H1	1801	2056
39	228864.5.dec	2438735H1	224	437	41	481454.4.dec	725929H1	1808	2056
39	228864.5.dec	4839445H1	263	537	41	481454.4.dec	710840H1	1834	2089
39	228864.5.dec	4698944H1	319	576	41	481454.4.dec	6554952H1	1852	2375
39	228864.5.dec	503758H1	322	558	41	481454.4.dec	192279F1	1854	2273
39	228864.5.dec	516461H1	383	598	41	481454.4.dec	1262802H1	1370	1565
39	228864.5.dec	2413301H1	387	600	41	481454.4.dec	722414H1	1357	1609
39	228864.5.dec	873275T1	414	714	41	481454.4.dec	1262803H1	1371	1564
39	228864.5.dec	873275H1	414	652	41	481454.4.dec	727709H1	1400	1616
39	228864.5.dec	g2166848	1	514	41	481454.4.dec	368161H1	1410	1671
39	228864.5.dec	6513978H1	1	543	41	481454.4.dec	3248182H1	1469	1738
39	228864.5.dec	3321280H1	1	259	41	481454.4.dec	192279H1	1490	1712
39	228864.5.dec	3537292H1	4	270	41	481454.4.dec	192279R1	1490	2004
39	228864.5.dec	3974316H1	4	291	41	481454.4.dec	719958H1	1502	1720
39	228864.5.dec	6269744H1	15	506	41	481454.4.dec	710004H1	1504	1741
39	228864.5.dec	2276784H1	27	263	41	481454.4.dec	1386020H1	1525	1696
39	228864.5.dec	2707203H1	175	414	41	481454.4.dec	720247H1	1527	1699
39	228864.5.dec	4317110H1	176	452	41	481454.4.dec	1423446H1	320	467
39	228864.5.dec	5106358H1	184	430	41	481454.4.dec	3214020H1	320	574
39	228864.5.dec	1886806H1	214	487	41	481454.4.dec	2991370F6	318	524
39	228864.5.dec	g1576711	215	374	41	481454.4.dec	1387254H1	320	529
39	228864.5.dec	604541H1	217	436	41	481454.4.dec	1387640H1	317	456
40	986539.1.dec	g4085132	256	725	41	481454.4.dec	2991370H1	318	557
40	986539.1.dec	g4222648	263	598	41	481454.4.dec	712619H1	191	315
40	986539.1.dec	g865178	246	530	41	481454.4.dec	3346330H1	312	593
40	986539.1.dec	6432233H1	247	648	41	481454.4.dec	1261236H1	317	566
40	986539.1.dec	g1064176	290	601	41	481454.4.dec	1261236R1	317	795
40	986539.1.dec	g3053295	238	600	41	481454.4.dec	6316533H1	1	301
40	986539.1.dec	g2912341	305	686	41	481454.4.dec	4773101H1	2287	2413
40	986539.1.dec	g2902568	310	466	41	481454.4.dec	3388764H1	1107	1386
40	986539.1.dec	g1757251	1	415	41	481454.4.dec	3738442H1	1747	1982
40	986539.1.dec	g4888422	1	226	41	481454.4.dec	1363446F1	1763	2199
40	986539.1.dec	g2898861	314	596	41	481454.4.dec	1363446H1	1763	2019
40	986539.1.dec	g1678784	547	937	41	481454.4.dec	359082H1	1766	2003
40	986539.1.dec	6160421H1	549	835	41	481454.4.dec	3251870H1	1770	1882
40	986539.1.dec	g2526384	20	245	41	481454.4.dec	1422809H1	1031	1280
40	986539.1.dec	493287H1	202	416	41	481454.4.d c	3550570H1	1045	1177
40	986539.1.dec	4433535H1	640	912	41	481454.4.dec	3553072H1	1063	1360
40	986539.1.dec	g2714767	732	1240	41	481454.4.dec	4243360H1	1106	1229
40	986539.1.dec	g2703735	789	1257	41	481454.4.dec	2495808H1	1863	2212
41	481454.4.dec	3552820H1	1124	1408	41	481454.4.dec	708530H1	1874	2093
41	481454.4.d c	4239624H1	980	1237	41	481454.4.dec	720746H1	1869	2087
41	481454.4.dec	727425H1	998	1225	41	481454.4.dec	719117H1	1919	2136

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41	481454.4.dec	724019H1	1933	2141
41	481454.4.dec	1388274H1	1942	2188
41	481454.4.dec	719545H1	1949	2145
41	481454.4.dec	g831279	2034	2426
41	481454.4.dec	g891552	2051	2395
41	481454.4.dec	g646749	2091	2375
41	481454.4.dec	g2017804	2144	2380
41	481454.4.dec	5375110H1	2201	2372
41	481454.4.dec	1262647H1	750	980
41	481454.4.dec	1262647R6	750	1196
41	481454.4.dec	3551542H1	899	1196
41	481454.4.dec	725130R6	961	1399
41	481454.4.dec	725130H1	961	1242
41	481454.4.dec	190292F1	976	1504
41	481454.4.dec	190292H1	371	594
41	481454.4.dec	190292R1	372	916
41	481454.4.dec	1388249H1	415	641
41	481454.4.dec	2987096H1	441	526
41	481454.4.dec	g573061	462	781
41	481454.4.dec	721632H1	495	734
41	481454.4.dec	5896660H1	537	816
41	481454.4.dec	4028467H1	583	831
41	481454.4.dec	3551808H1	627	915
41	481454.4.dec	g694536	683	922
41	481454.4.dec	3552507H1	730	1009
41	481454.4.dec	1262647R1	750	1243
41	481454.4.dec	2534573H1	1163	1277
41	481454.4.dec	664692H1	1187	1371
41	481454.4.dec	3739532H1	1345	1520
42	474800.7.dec	g4083621	348	790
42	474800.7.dec	g3330186	352	795
42	474800.7.dec	g4006598	353	796
42	474800.7.dec	g3154709	368	791
42	474800.7.dec	1376567F1	360	789
42	474800.7.dec	3866046H1	360	634
42	474800.7.dec	1376567H1	360	600
42	474800.7.dec	4454657H1	367	565
42	474800.7.dec	g1422686	367	791
42	474800.7.dec	g1698074	370	787
42	474800.7.dec	g3424851	373	789
42	474800.7.dec	6006731H1	376	568
42	474800.7.dec	2191974H1	263	506
42	474800.7.dec	3436827H1	265	507
42	474800.7.dec	2947062H2	261	528
42	474800.7.dec	3471528H1	261	448
42	474800.7.dec	2095746H1	261	520
42	474800.7.dec	g2063997	262	716
42	474800.7.dec	4300620H1	264	521
42	474800.7.dec	2452854H1	263	511
42	474800.7.dec	2365057H1	263	496
42	474800.7.dec	1643560H1	263	471
42	474800.7.dec	1514783H1	263	444
42	474800.7.dec	4386745H1	264	509
42	474800.7.dec	3624130H1	262	505
42	474800.7.dec	3968293H1	262	538
42	474800.7.dec	575286H1	264	564
42	474800.7.dec	1347134H1	265	499
42	474800.7.dec	g1642050	266	548
42	474800.7.dec	3182016H1	267	575
42	474800.7.dec	4979746H1	267	534
42	474800.7.dec	g1698167	259	567
42	474800.7.dec	1467071H1	259	457
42	474800.7.dec	g1067573	261	490
42	474800.7.dec	4556026H1	261	520
42	474800.7.dec	2367365H1	260	497
42	474800.7.dec	1004773H1	261	448
42	474800.7.dec	1493863H1	283	506
42	474800.7.dec	g894785	284	381
42	474800.7.dec	3364132H1	285	506
42	474800.7.dec	6296402H1	282	393
42	474800.7.dec	g759692	285	481
42	474800.7.d c	g2269717	284	342
42	474800.7.dec	4800860H1	283	541
42	474800.7.dec	5866864H1	285	454
42	474800.7.dec	4974548H1	287	558
42	474800.7.dec	671748H1	288	536
42	474800.7.dec	4626725H1	290	553
42	474800.7.dec	4549937H1	291	517
42	474800.7.dec	702403H1	292	523
42	474800.7.dec	3085429H1	292	574
42	474800.7.dec	2536581H1	297	554
42	474800.7.dec	4577417H1	297	558
42	474800.7.dec	3278477H1	302	559
42	474800.7.dec	3525826H1	302	636
42	474800.7.dec	2274935H1	273	527
42	474800.7.dec	6128496H1	276	781
42	474800.7.dec	3538467H1	251	452
42	474800.7.dec	g1696705	255	716
42	474800.7.dec	4654475H1	254	517
42	474800.7.dec	2519031H1	253	485
42	474800.7.dec	1415905H1	253	339
42	474800.7.dec	g1991337	254	556
42	474800.7.dec	6128132H1	256	770
42	474800.7.dec	6512254H1	256	764
42	474800.7.dec	861646T1	255	739
42	474800.7.dec	6127445H1	256	680
42	474800.7.dec	5921246H1	254	546
42	474800.7.dec	1754734H1	255	486
42	474800.7.dec	6154991H1	257	559
42	474800.7.dec	3162126H1	255	531
42	474800.7.dec	3435104H1	255	529
42	474800.7.dec	5170106H1	256	534
42	474800.7.dec	5118447H1	256	521
42	474800.7.dec	3493016H1	255	348
42	474800.7.dec	3551427H1	255	546
42	474800.7.dec	3148115H1	255	542
42	474800.7.dec	3318467H1	252	513
42	474800.7.dec	2271268H1	256	517
42	474800.7.dec	4548927H1	255	477
42	474800.7.dec	861653H1	255	491
42	474800.7.dec	3746336H1	256	525
42	474800.7.dec	3135584H1	257	518
42	474800.7.dec	5666988H1	257	458
42	474800.7.dec	2990527H1	255	554
42	474800.7.dec	g3736691	736	786
42	474800.7.dec	4903583H2	619	771
42	474800.7.dec	3375214H1	631	789
42	474800.7.dec	g2737517	634	789
42	474800.7.dec	g2184209	657	789
42	474800.7.dec	g2184197	658	789
42	474800.7.dec	g4088940	665	790
42	474800.7.dec	3731668H1	670	787
42	474800.7.dec	g3846489	676	789
42	474800.7.dec	g3307015	684	796
42	474800.7.dec	922106H1	683	789
42	474800.7.dec	g5232862	687	789
42	474800.7.dec	g1696663	699	789
42	474800.7.dec	g2408773	706	785
42	474800.7.dec	g2261612	729	789
42	474800.7.dec	g4075039	730	788
42	474800.7.dec	g1148234	732	810
42	474800.7.d c	4012655H1	239	532
42	474800.7.dec	2117980H1	239	554
42	474800.7.dec	5634457H1	239	478
42	474800.7.dec	2534090H1	241	480
42	474800.7.dec	2714824H1	238	465

Table 2 cont.

42	474800.7.dec	2210110H1	242	481
42	474800.7.dec	2215995H1	242	432
42	474800.7.d c	730002R1	244	587
42	474800.7.dec	3566922H1	239	451
42	474800.7.dec	3714080H1	244	549
42	474800.7.dec	g1954653	244	488
42	474800.7.dec	749975R1	247	706
42	474800.7.dec	1259725F1	247	535
42	474800.7.dec	4834575H1	248	515
42	474800.7.dec	730002H1	244	464
42	474800.7.dec	2434564H1	244	460
42	474800.7.dec	4514277H1	246	501
42	474800.7.dec	2494966F6	246	721
42	474800.7.dec	2149266H1	246	506
42	474800.7.dec	2729518H1	246	495
42	474800.7.dec	2211220H1	246	488
42	474800.7.dec	1696726H1	235	449
42	474800.7.dec	1462849H1	239	433
42	474800.7.dec	2494966H1	246	475
42	474800.7.dec	4957528H1	246	515
42	474800.7.dec	2893665H1	246	530
42	474800.7.dec	2208894H1	246	512
42	474800.7.dec	4803367H1	248	508
42	474800.7.dec	2480259H1	246	472
42	474800.7.dec	402691H1	246	328
42	474800.7.dec	4079809H1	247	508
42	474800.7.dec	3180571H1	247	527
42	474800.7.dec	1357326F1	248	508
42	474800.7.dec	4952010H1	248	503
42	474800.7.dec	1918861H1	247	498
42	474800.7.dec	662273H1	248	512
42	474800.7.dec	1357326H1	248	480
42	474800.7.dec	5669715H1	244	421
42	474800.7.dec	606874H1	247	499
42	474800.7.dec	1591056H1	232	422
42	474800.7.dec	1286616H1	234	488
42	474800.7.dec	1286624H1	234	483
42	474800.7.dec	4731307H1	232	498
42	474800.7.dec	3749645H1	281	508
42	474800.7.dec	1922474H1	280	517
42	474800.7.dec	1340372H1	283	524
42	474800.7.dec	6178119H1	283	560
42	474800.7.dec	1729885H1	235	456
42	474800.7.dec	1294227H1	234	463
42	474800.7.dec	g1324145	238	685
42	474800.7.dec	1295132H1	234	368
42	474800.7.dec	3805569H1	237	507
42	474800.7.dec	4663018H1	237	494
42	474800.7.dec	2372879H1	237	469
42	474800.7.dec	4459840H1	232	488
42	474800.7.dec	4020679H1	234	364
42	474800.7.dec	1970955H1	235	482
42	474800.7.dec	3140080H1	232	462
42	474800.7.dec	3270140H1	232	472
42	474800.7.dec	2501703H1	232	452
42	474800.7.dec	5849717H1	234	525
42	474800.7.dec	1294427H1	234	452
42	474800.7.dec	2607262H1	235	489
42	474800.7.dec	2494702H1	232	539
42	474800.7.dec	3015135H1	232	386
42	474800.7.dec	1338720H1	276	508
42	474800.7.dec	1551538H1	276	483
42	474800.7.dec	1530539H1	276	454
42	474800.7.dec	2993256H1	277	577
42	474800.7.dec	5426861H1	276	481
42	474800.7.d c	2995818H1	276	507
42	474800.7.dec	5281131H1	277	482
42	474800.7.dec	4702690H1	277	400
42	474800.7.dec	3976719H1	278	552
42	474800.7.dec	g844775	482	790
42	474800.7.dec	g4629548	553	789
42	474800.7.dec	g1137292	551	789
42	474800.7.d c	6296919H1	483	789
42	474800.7.dec	g3887267	486	773
42	474800.7.dec	g3894445	489	773
42	474800.7.dec	3733891H1	502	789
42	474800.7.dec	6348720H1	503	788
42	474800.7.dec	1235676F1	515	797
42	474800.7.dec	1235676H1	515	791
42	474800.7.dec	5268670H1	523	630
42	474800.7.dec	2884366H1	555	789
42	474800.7.dec	1372524H1	556	779
42	474800.7.dec	1349872F1	525	789
42	474800.7.dec	4115166H1	558	794
42	474800.7.dec	1349872H1	525	773
42	474800.7.dec	5269780H1	523	676
42	474800.7.dec	2752779H1	538	787
42	474800.7.dec	g895371	558	787
42	474800.7.dec	g4147221	545	789
42	474800.7.dec	6096488H1	581	801
42	474800.7.dec	155808H1	592	785
42	474800.7.dec	g1728642	549	787
42	474800.7.dec	g812572	603	785
42	474800.7.dec	2494966T6	603	753
42	474800.7.dec	g2184440	610	771
42	474800.7.dec	g2184427	611	771
42	474800.7.dec	g4149309	617	789
42	474800.7.dec	3933576H1	248	530
42	474800.7.dec	749975H1	247	482
42	474800.7.dec	1260232H1	247	474
42	474800.7.dec	1259725H1	247	460
42	474800.7.dec	2906023H1	248	543
42	474800.7.dec	3136046H1	248	514
42	474800.7.dec	3401103H1	248	498
42	474800.7.dec	3457224H2	248	494
42	474800.7.dec	4820352H1	249	520
42	474800.7.dec	4152618H1	247	500
42	474800.7.dec	3297825H1	247	495
42	474800.7.dec	1211350H1	248	499
42	474800.7.dec	5279226H1	247	490
42	474800.7.dec	3719225H1	248	533
42	474800.7.dec	5276645H1	249	491
42	474800.7.dec	4068071H1	248	509
42	474800.7.dec	4627628H1	248	495
42	474800.7.dec	3858350H1	249	364
42	474800.7.dec	4983991H1	249	498
42	474800.7.dec	2723389H1	248	473
42	474800.7.dec	6175731H1	276	540
42	474800.7.dec	924412H1	276	526
42	474800.7.dec	4274039H1	276	567
42	474800.7.dec	4158452H1	276	507
42	474800.7.dec	g834460	276	549
42	474800.7.dec	1231788H1	274	505
42	474800.7.dec	3925434H1	276	382
42	474800.7.dec	g2037450	277	596
42	474800.7.dec	227482R1	277	790
42	474800.7.dec	924412R1	276	651
42	474800.7.dec	989831H1	276	497
42	474800.7.dec	3095592H1	276	567
42	474800.7.dec	2847487H1	276	534
42	474800.7.dec	5212828H1	276	522
42	474800.7.dec	2765830H1	276	501
42	474800.7.dec	925174H1	276	578
42	474800.7.dec	5168959H1	255	490
42	474800.7.dec	5986292H1	253	512
42	474800.7.dec	1966146H1	253	484

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42	474800.7.dec	2289883H1	253	479
42	474800.7.dec	2424789H1	252	497
42	474800.7.dec	4166923H1	254	549
42	474800.7.dec	4373163H1	254	508
42	474800.7.d c	989826T1	276	745
42	474800.7.dec	6268931H1	276	657
42	474800.7.dec	1813453H1	276	542
42	474800.7.dec	4670644H1	276	538
42	474800.7.dec	3715127H1	276	509
42	474800.7.dec	g1422739	276	625
42	474800.7.dec	899948H1	274	582
42	474800.7.dec	4356250H1	275	541
42	474800.7.dec	4858015H1	276	531
42	474800.7.dec	5079276H1	276	522
42	474800.7.dec	1613653H1	332	483
42	474800.7.dec	3402418H1	336	560
42	474800.7.dec	g4531872	337	788
42	474800.7.dec	3137321H1	335	606
42	474800.7.dec	g704952	337	609
42	474800.7.dec	1866326H1	342	600
42	474800.7.dec	1922984H1	342	588
42	474800.7.dec	g3594118	1	183
42	474800.7.dec	g2524860	1	290
42	474800.7.dec	1930667H1	1	273
42	474800.7.dec	g2011957	8	222
42	474800.7.dec	1733892H1	36	258
42	474800.7.dec	3505415H1	52	349
42	474800.7.dec	1700409H1	115	319
42	474800.7.dec	1700409F6	115	541
42	474800.7.dec	5027694H1	184	409
42	474800.7.dec	1517060H1	214	417
42	474800.7.dec	4844124H1	217	466
42	474800.7.dec	4016409H1	218	362
42	474800.7.dec	4702861H1	217	460
42	474800.7.dec	2523175H1	217	465
42	474800.7.dec	5304920H1	223	404
42	474800.7.dec	2366003H1	223	458
42	474800.7.dec	3780782H1	226	535
42	474800.7.dec	996082H1	228	377
42	474800.7.dec	822805R1	227	793
42	474800.7.dec	1996347R6	232	637
42	474800.7.dec	3093975H1	232	515
42	474800.7.dec	3133938H1	232	511
42	474800.7.dec	6381463H1	232	529
42	474800.7.dec	1996347H1	232	496
42	474800.7.dec	2861204H1	232	498
42	474800.7.dec	4898341H1	232	520
42	474800.7.dec	2495973H1	232	476
42	474800.7.dec	1970513H1	263	508
42	474800.7.dec	2256505H1	261	522
42	474800.7.dec	2522247H1	261	516
42	474800.7.dec	g1153120	260	641
42	474800.7.dec	6152879H1	262	552
42	474800.7.dec	3036532H1	262	543
42	474800.7.dec	4545977H1	262	525
42	474800.7.dec	3948286H1	262	512
42	474800.7.dec	4752453H1	262	502
42	474800.7.dec	6181894H1	267	538
42	474800.7.dec	3575944H1	267	562
42	474800.7.dec	2512525H1	267	490
42	474800.7.dec	g1320480	265	703
42	474800.7.dec	g1101165	268	574
42	474800.7.dec	3206634H1	266	509
42	474800.7.dec	g992293	269	561
42	474800.7.dec	752410H1	271	483
42	474800.7.dec	g1298225	273	445
42	474800.7.dec	3021579H1	271	561
42	474800.7.dec	3523078H1	271	536
42	474800.7.dec	3285384H1	271	524
42	474800.7.dec	3482242H1	271	573
42	474800.7.dec	1494042H1	272	447
42	474800.7.dec	1495315H1	272	377
42	474800.7.dec	899948R1	274	786
42	474800.7.dec	2919115H1	274	544
42	474800.7.dec	3960502H2	232	499
42	474800.7.dec	2583991H1	232	499
42	474800.7.dec	4898343H1	232	516
42	474800.7.dec	4708081H1	233	513
42	474800.7.dec	605146H1	232	509
42	474800.7.dec	960257H1	232	514
42	474800.7.dec	2661227H1	232	481
42	474800.7.dec	4108170H1	232	496
42	474800.7.dec	3238444H1	232	467
42	474800.7.dec	5079639H1	232	486
42	474800.7.dec	1360090H1	232	435
42	474800.7.dec	3359828H1	399	674
42	474800.7.dec	857142H1	404	627
42	474800.7.dec	2011561H1	417	605
42	474800.7.dec	g1266718	426	804
42	474800.7.dec	g1523438	425	794
42	474800.7.dec	g1264895	427	811
42	474800.7.dec	g1209924	428	787
42	474800.7.dec	5177460H1	436	706
42	474800.7.dec	4548929T1	440	746
42	474800.7.dec	g899619	442	786
42	474800.7.dec	g2017819	443	789
42	474800.7.dec	6054166H1	461	791
42	474800.7.dec	5115520H1	462	730
42	474800.7.dec	508565H1	465	704
42	474800.7.dec	1700409T6	466	751
42	474800.7.dec	g1010182	468	783
42	474800.7.dec	5421771H2	261	438
42	474800.7.dec	g907455	261	576
42	474800.7.dec	3047569H1	260	565
42	474800.7.dec	g834588	261	562
42	474800.7.dec	2564290H1	261	515
42	474800.7.dec	3979793H1	262	534
42	474800.7.dec	982280T2	263	751
42	474800.7.dec	982280H1	263	590
42	474800.7.dec	4987995H1	262	529
42	474800.7.dec	3762921H1	264	535
42	474800.7.dec	2455009H1	262	504
42	474800.7.dec	4773159H1	263	543
42	474800.7.dec	953978H1	262	511
42	474800.7.dec	1633657H1	262	480
42	474800.7.dec	2727526H1	262	491
42	474800.7.dec	4058979H1	262	426
42	474800.7.dec	799446H1	264	502
42	474800.7.dec	g1551980	261	441
42	474800.7.dec	2496135H1	264	580
42	474800.7.dec	2811787H1	263	542
42	474800.7.dec	3360431H1	263	531
42	474800.7.dec	4773156H1	276	560
42	474800.7.dec	4379475H1	277	548
42	474800.7.dec	g1551620	276	379
42	474800.7.dec	2912032H1	276	544
42	474800.7.dec	2632654H1	276	532
42	474800.7.dec	3401603H1	276	530
42	474800.7.dec	3317001H1	276	530
42	474800.7.dec	2768258H1	276	516
42	474800.7.dec	g844830	228	557
42	474800.7.dec	g1200612	225	517
42	474800.7.dec	996082R1	228	785
42	474800.7.dec	1418641H1	228	485
42	474800.7.dec	1418610H1	228	478
42	474800.7.dec	822805H1	227	446

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42	474800.7.dec	1571453H1	227	331	42	474800.7.dec	g1069389	248	570
42	474800.7.dec	3450482H1	229	475	42	474800.7.dec	4718186H1	250	513
42	474800.7.dec	4297547H1	229	404	42	474800.7.d c	2507696H1	249	481
42	474800.7.dec	1982331H1	228	506	42	474800.7.dec	832375H1	249	338
42	474800.7.dec	2078474H1	228	493	42	474800.7.dec	3384841H1	250	477
42	474800.7.dec	4655615H1	228	494	42	474800.7.dec	3090981H1	248	514
42	474800.7.dec	4718836H1	228	501	42	474800.7.dec	2496134H1	247	476
42	474800.7.dec	2748984H1	228	490	42	474800.7.dec	2070351H1	251	468
42	474800.7.dec	2725538H1	228	477	42	474800.7.dec	3343389H1	251	497
42	474800.7.dec	2688345H1	228	477	42	474800.7.dec	2328523H1	251	502
42	474800.7.dec	5260612H1	228	452	42	474800.7.dec	1540212H1	281	501
42	474800.7.dec	2828878H1	261	526	42	474800.7.dec	1664483H1	281	493
42	474800.7.dec	3352277H1	261	513	42	474800.7.dec	g1954939	283	528
42	474800.7.dec	5438786H1	262	537	42	474800.7.dec	1652595H1	281	504
42	474800.7.dec	608875H1	260	498	42	474800.7.dec	3256087H1	282	517
42	474800.7.dec	g1687582	259	507	42	474800.7.dec	2664505H1	276	511
42	474800.7.dec	2528382H1	262	582	42	474800.7.dec	3133484H1	276	560
42	474800.7.dec	3161323H1	261	560	42	474800.7.dec	902991H1	274	443
42	474800.7.dec	3815719H1	262	552	42	474800.7.dec	2523971H1	274	457
42	474800.7.dec	5927826H1	261	552	42	474800.7.dec	4065211H1	277	554
42	474800.7.dec	2103114H1	261	524	42	474800.7.dec	5847748H1	277	555
42	474800.7.dec	5685850H1	304	457	42	474800.7.dec	3241608H1	277	521
42	474800.7.dec	g869962	317	521	42	474800.7.dec	1558275H1	228	438
42	474800.7.dec	g3446179	319	765	42	474800.7.dec	3945726H1	230	521
42	474800.7.dec	207985H1	323	566	42	474800.7.dec	3864787H1	224	382
42	474800.7.dec	2321546H1	323	562	42	474800.7.dec	5993349H1	230	506
42	474800.7.dec	4863479H1	333	572	42	474800.7.dec	4304036H1	229	481
42	474800.7.dec	g2540814	332	813	42	474800.7.dec	4359071H1	231	441
42	474800.7.dec	4503887H1	333	579	42	474800.7.dec	759905H1	228	443
42	474800.7.dec	g3679347	335	790	42	474800.7.dec	626533H1	232	480
42	474800.7.dec	4501531H1	333	498	42	474800.7.dec	4359017H1	230	499
42	474800.7.dec	227482H1	276	386	42	474800.7.dec	4160125H1	231	486
42	474800.7.dec	2864302H1	278	601	42	474800.7.dec	605146R1	232	789
42	474800.7.dec	4667387H1	280	536	42	474800.7.dec	641045H1	231	487
42	474800.7.dec	4587242H1	280	535	42	474800.7.dec	4774994H1	228	473
42	474800.7.dec	4013223H1	280	568	42	474800.7.dec	g1275341	231	726
42	474800.7.dec	4364726H1	281	536	42	474800.7.dec	5218085H1	232	489
42	474800.7.dec	5585051H1	281	508	42	474800.7.dec	1581422H1	231	414
42	474800.7.dec	g1614356	276	430	42	474800.7.dec	2875181H1	231	416
42	474800.7.dec	5292222H2	281	476	42	474800.7.dec	4108876H1	232	509
42	474800.7.dec	4014021H1	281	555	42	474800.7.dec	763465H1	232	458
42	474800.7.dec	1996347T6	283	749	42	474800.7.dec	1360090F1	232	712
42	474800.7.dec	2603087H1	282	565	43	427883.13.dec	2750357R6	1	585
42	474800.7.dec	2726460H1	283	533	43	427883.13.dec	2750357H1	1	274
42	474800.7.dec	2520565H1	282	530	43	427883.13.dec	2750357T6	66	600
42	474800.7.dec	g3648049	382	787	43	427883.13.dec	g2145067	177	680
42	474800.7.dec	g3785151	392	789	44	018945.1.dec	g2754249	148	381
42	474800.7.dec	g4621991	392	788	44	018945.1.dec	6316156H1	1	265
42	474800.7.dec	4548927T1	396	746	44	018945.1.dec	2494157F6	100	578
42	474800.7.dec	2417032H1	256	496	44	018945.1.dec	5926973H1	260	527
42	474800.7.dec	2458318H1	256	473	44	018945.1.dec	5843114H1	340	556
42	474800.7.dec	g899701	257	366	44	018945.1.dec	2494157H1	101	374
42	474800.7.dec	g1925616	260	686	44	018945.1.dec	3332135H1	103	272
42	474800.7.dec	2423152H1	257	496	45	353271.2.dec	g2166108	1	268
42	474800.7.dec	g1969694	259	528	45	353271.2.dec	g1982479	27	253
42	474800.7.dec	g1991227	259	523	45	353271.2.dec	1330982H1	1	223
42	474800.7.dec	3984471H1	258	526	45	353271.2.dec	g656570	46	300
42	474800.7.dec	3797251H1	256	420	45	353271.2.dec	6264802H1	166	684
42	474800.7.dec	2515639H1	256	377	45	353271.2.dec	g5393964	500	874
42	474800.7.dec	1982495H1	258	434	45	353271.2.dec	g2817460	555	977
42	474800.7.dec	3384040H1	258	518	45	353271.2.dec	g3144408	555	951
42	474800.7.dec	4340308H1	262	520	45	353271.2.dec	g2884545	555	872
42	474800.7.dec	5485719H2	263	536	45	353271.2.dec	6433345H1	685	1075
42	474800.7.dec	3399655H1	249	488	46	221686.2.dec	g1496021	950	1174
42	474800.7.d c	4079842H1	247	504	46	221686.2.dec	2222469H1	980	1228
42	474800.7.dec	g2018263	248	489	46	221686.2.dec	3702201H1	4	224
42	474800.7.dec	3595893H1	250	545	46	221686.2.dec	2869444H1	5	267
42	474800.7.dec	4353689H1	248	466	46	221686.2.dec	2608081H1	5	239

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46	221686.2.dec	2560547H1	20	262
46	221686.2.dec	865274H1	20	229
46	221686.2.dec	4600487H1	1207	1471
46	221686.2.dec	g5395617	1212	1658
46	221686.2.d c	g3649326	1197	1649
46	221686.2.dec	1924003H1	1205	1440
46	221686.2.dec	g2229467	786	1285
46	221686.2.dec	6560891H1	824	1412
46	221686.2.dec	4309204H1	840	1156
46	221686.2.dec	g1894676	847	1068
46	221686.2.dec	1320608H1	739	977
46	221686.2.dec	1322509H1	739	1012
46	221686.2.dec	g1962089	742	1161
46	221686.2.dec	g1501804	748	1240
46	221686.2.dec	277812H1	759	997
46	221686.2.dec	891686R1	780	1232
46	221686.2.dec	891686H1	780	1057
46	221686.2.dec	6541682H1	785	835
46	221686.2.dec	2757069H1	4	264
46	221686.2.dec	3371090H1	4	191
46	221686.2.dec	g1157161	1	376
46	221686.2.dec	3269337H1	1	230
46	221686.2.dec	3744013H1	3	291
46	221686.2.dec	g1648248	4	321
46	221686.2.dec	2755673H1	4	281
46	221686.2.dec	4539363H1	1297	1532
46	221686.2.dec	4539354H1	1296	1529
46	221686.2.dec	g877030	439	821
46	221686.2.dec	g3085798	403	565
46	221686.2.dec	602072H1	443	649
46	221686.2.dec	g4089352	1282	1649
46	221686.2.dec	g3424232	1285	1655
46	221686.2.dec	g618384	1287	1649
46	221686.2.dec	g899949	1295	1662
46	221686.2.dec	5214483H1	1217	1473
46	221686.2.dec	g2904724	1219	1648
46	221686.2.dec	4840724H1	1484	1649
46	221686.2.dec	2291586H1	1491	1648
46	221686.2.dec	g3597611	1529	1654
46	221686.2.dec	g2252086	1536	1657
46	221686.2.dec	g3069279	1555	1661
46	221686.2.dec	g4619485	1571	1649
46	221686.2.dec	g4285953	1465	1649
46	221686.2.dec	g2670165	1480	1649
46	221686.2.dec	2191582H1	1	245
46	221686.2.dec	1758533T6	1	526
46	221686.2.dec	5023657H1	949	1287
46	221686.2.dec	5004265H1	1308	1451
46	221686.2.dec	g2944918	1313	1656
46	221686.2.dec	g1521805	1315	1649
46	221686.2.dec	g3281247	1315	1649
46	221686.2.dec	g4111170	1322	1648
46	221686.2.dec	g678095	1328	1649
46	221686.2.dec	g3239905	1365	1652
46	221686.2.dec	3009995H1	1365	1654
46	221686.2.dec	2768117H1	75	324
46	221686.2.dec	g2056693	90	482
46	221686.2.dec	1914093H1	43	290
46	221686.2.dec	g5664064	104	570
46	221686.2.dec	6555452H1	1084	1647
46	221686.2.dec	1985587H1	1099	1349
46	221686.2.dec	2794944H1	1118	1379
46	221686.2.dec	4765822H1	329	635
46	221686.2.dec	g3434809	1280	1649
46	221686.2.dec	3492290H1	227	509
46	221686.2.dec	g2464021	229	563
46	221686.2.dec	g1139048	253	564
46	221686.2.dec	g2057237	258	564
46	221686.2.dec	g1970171	278	529
46	221686.2.dec	g3050156	319	551
46	221686.2.dec	g5393393	196	551
46	221686.2.dec	g4390118	200	564
46	221686.2.dec	g4311801	205	549
46	221686.2.dec	g2986647	221	567
46	221686.2.dec	g3134329	222	564
46	221686.2.dec	2192270H1	506	567
46	221686.2.dec	3972831F8	584	948
46	221686.2.dec	g1847092	601	656
46	221686.2.dec	6064569H1	613	903
46	221686.2.dec	g565892	508	785
46	221686.2.dec	g705571	508	765
46	221686.2.dec	g900050	543	821
46	221686.2.dec	g2110278	551	941
46	221686.2.dec	3644153H1	563	845
46	221686.2.dec	3972831H1	584	763
46	221686.2.dec	5264943H2	583	842
46	221686.2.dec	g1496022	1224	1649
46	221686.2.dec	2276917H1	1233	1474
46	221686.2.dec	g2223945	448	564
46	221686.2.dec	g748720	489	816
46	221686.2.dec	508694H1	492	564
46	221686.2.dec	g3871207	494	594
46	221686.2.dec	1449534H1	501	725
46	221686.2.dec	g3599990	20	1649
46	221686.2.dec	3212603H1	20	96
46	221686.2.dec	2692989H1	20	234
46	221686.2.dec	1524060H1	20	242
46	221686.2.dec	g876029	24	337
46	221686.2.dec	2350967H1	33	240
46	221686.2.dec	505094H1	1125	1343
46	221686.2.dec	4349946H1	1169	1409
46	221686.2.dec	g5368644	1449	1654
46	221686.2.dec	2561462H1	1461	1653
46	221686.2.dec	4338064H1	1065	1199
46	221686.2.dec	6555559H1	1084	1397
46	221686.2.dec	g5100441	115	567
46	221686.2.dec	g4244273	120	567
46	221686.2.dec	g4598846	121	566
46	221686.2.dec	g5525897	126	569
46	221686.2.dec	g4222849	137	564
46	221686.2.dec	g1940783	96	481
46	221686.2.dec	g4683228	149	602
46	221686.2.dec	g1966888	171	591
46	221686.2.dec	g3230774	1188	1656
46	221686.2.dec	g5235938	1190	1653
46	221686.2.dec	g2335846	1189	1653
46	221686.2.dec	1945431H1	50	284
46	221686.2.dec	2351607H1	33	272
46	221686.2.dec	g2220565	27	476
46	221686.2.dec	g2179118	1257	1635
46	221686.2.dec	4545185H1	874	1109
46	221686.2.dec	3614865H1	887	1183
46	221686.2.dec	1758533R6	7	398
46	221686.2.dec	1758533H1	7	260
46	221686.2.dec	2520988H1	7	239
46	221686.2.dec	6570842H1	999	1535
46	221686.2.dec	g2229468	1180	1654
46	221686.2.dec	g1501805	1189	1649
46	221686.2.dec	843100R1	1004	1565
46	221686.2.dec	843100H1	1004	1251
46	221686.2.dec	1322509T6	1012	1608
46	221686.2.dec	2865824H1	17	312
46	221686.2.dec	3494081H1	20	141
46	221686.2.dec	3421965H1	20	225
46	221686.2.dec	g3180993	171	573
46	221686.2.dec	4200256H1	185	456

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46	221686.2.dec	g3053185	193	551	47	233347.7.dec	628818H1	867	1114
46	221686.2.dec	g4113264	194	564	47	233347.7.dec	5550441H1	872	1115
46	221686.2.dec	1566145H1	215	413	47	233347.7.dec	621350H1	882	1148
46	221686.2.dec	4146653H1	658	905	47	233347.7.dec	5855889H1	892	1196
46	221686.2.dec	g2038320	661	1012	47	233347.7.dec	g4331585	896	1242
46	221686.2.dec	870643R1	688	1236	47	233347.7.dec	1997765R6	901	1211
46	221686.2.dec	870643H1	688	904	47	233347.7.dec	1997765H1	901	1109
46	221686.2.dec	2472630H1	739	966	47	233347.7.dec	6117878H1	901	1166
46	221686.2.dec	5642893H1	1274	1526	47	233347.7.dec	2241265H1	908	1159
46	221686.2.dec	g4089330	1259	1654	47	233347.7.dec	g2969034	916	1311
46	221686.2.dec	g1874878	617	1032	47	233347.7.dec	4509861H1	920	1178
46	221686.2.dec	g760468	624	899	47	233347.7.dec	5075055H1	931	1179
46	221686.2.dec	g1875083	643	1064	47	233347.7.dec	1724406H1	948	1159
46	221686.2.dec	4115809H1	648	946	47	233347.7.dec	3074869H1	948	1226
46	221686.2.dec	2190470H1	654	899	47	233347.7.dec	g1158164	953	1291
46	221686.2.dec	g5365668	1242	1649	47	233347.7.dec	2506817T6	953	1554
46	221686.2.dec	g3665314	1246	1649	47	233347.7.dec	1683282T7	953	1563
46	221686.2.dec	g4896697	1251	1655	47	233347.7.dec	1444691H1	955	1205
46	221686.2.dec	g4682121	1255	1650	47	233347.7.dec	5201751H1	956	1202
46	221686.2.dec	g5101618	1256	1648	47	233347.7.dec	2275646H1	973	1234
46	221686.2.dec	g3254734	1239	1649	47	233347.7.dec	2275638H1	973	1234
46	221686.2.dec	837519H1	1234	1475	47	233347.7.dec	572758H1	987	1235
46	221686.2.dec	g2110810	1235	1650	47	233347.7.dec	1997765T6	994	1557
46	221686.2.dec	6414447H1	1236	1649	47	233347.7.dec	2005649H1	996	1109
46	221686.2.dec	1322509F6	739	1200	47	233347.7.dec	2995962H1	997	1285
46	221686.2.dec	5327256H1	1195	1444	47	233347.7.dec	4668682H1	1002	1269
46	221686.2.dec	g1521860	1194	1578	47	233347.7.dec	5024735H1	1020	1310
46	221686.2.dec	1544501H1	17	139	47	233347.7.dec	g1137365	1021	1291
46	221686.2.dec	2458467H1	17	248	47	233347.7.dec	4029754T6	1024	1572
46	221686.2.dec	2494070H1	16	325	47	233347.7.dec	2879058T6	1026	1563
46	221686.2.dec	1503112H1	1379	1654	47	233347.7.dec	782138T6	1026	1556
46	221686.2.dec	g3871897	1386	1649	47	233347.7.dec	2882223T6	1028	1558
46	221686.2.dec	g3085806	1397	1649	47	233347.7.dec	2048496H1	1053	1298
46	221686.2.dec	g682225	1421	1649	47	233347.7.dec	2855651H1	1053	1311
46	221686.2.dec	g561064	1440	1649	47	233347.7.dec	2095114H1	1053	1353
46	221686.2.dec	g5707032	338	567	47	233347.7.dec	2882168T6	1063	1558
46	221686.2.dec	1871308H1	344	634	47	233347.7.dec	2132811T6	1063	1335
46	221686.2.dec	2253510H1	379	623	47	233347.7.dec	690448H1	1089	1330
46	221686.2.dec	3492962H1	395	688	47	233347.7.dec	2667831F6	1099	1590
47	233347.7.dec	5093226H1	104	380	47	233347.7.dec	2667777H1	1099	1325
47	233347.7.dec	6296882H1	552	874	47	233347.7.dec	4645421H1	1099	1333
47	233347.7.dec	g1956049	577	801	47	233347.7.dec	g3094666	1101	1492
47	233347.7.dec	2280565H1	546	834	47	233347.7.dec	136644F1	1111	1602
47	233347.7.dec	4950593H1	586	853	47	233347.7.dec	g3279211	1126	1597
47	233347.7.dec	g1266199	589	873	47	233347.7.dec	g5393561	1127	1598
47	233347.7.dec	2582086H1	111	347	47	233347.7.dec	g2328918	1131	1603
47	233347.7.dec	3289913H1	71	344	47	233347.7.dec	g3801124	1137	1602
47	233347.7.dec	5481292H1	76	250	47	233347.7.dec	6131567H1	1141	1234
47	233347.7.dec	1483352H1	76	361	47	233347.7.dec	3522523H1	1140	1478
47	233347.7.dec	2958439H1	61	356	47	233347.7.dec	g4150559	1155	1607
47	233347.7.dec	5174119H1	104	367	47	233347.7.dec	1864389T6	1155	1557
47	233347.7.dec	573115H1	103	344	47	233347.7.dec	5584776H1	1156	1286
47	233347.7.dec	4110287H1	737	960	47	233347.7.dec	747304H1	1157	1381
47	233347.7.dec	g1635141	741	921	47	233347.7.dec	841354H1	1167	1334
47	233347.7.dec	g2027455	749	1024	47	233347.7.dec	841354R1	1167	1602
47	233347.7.dec	3468767H1	749	936	47	233347.7.dec	2667831T6	1171	1560
47	233347.7.dec	g1101060	760	1049	47	233347.7.dec	3883246H1	1169	1414
47	233347.7.dec	2747911H1	767	1018	47	233347.7.dec	1996207H1	1172	1433
47	233347.7.dec	1335579H1	784	1038	47	233347.7.dec	g660429	1178	1385
47	233347.7.dec	3280038H1	785	1010	47	233347.7.dec	1420378H1	1181	1407
47	233347.7.dec	1394941H1	785	1055	47	233347.7.dec	g3797815	1193	1605
47	233347.7.dec	2485558H1	788	999	47	233347.7.d c	g4094464	1196	1593
47	233347.7.dec	1441111H1	796	1029	47	233347.7.dec	g3595501	1195	1475
47	233347.7.dec	1864633H1	795	1069	47	233347.7.dec	g1211828	1199	1598
47	233347.7.dec	5289668H1	800	1044	47	233347.7.d c	g3922052	1197	1605
47	233347.7.dec	632354H1	814	1069	47	233347.7.dec	g3280797	1196	1604
47	233347.7.dec	1432029H1	821	1058	47	233347.7.dec	053627H1	1198	1348
47	233347.7.dec	1690635H1	862	1159	47	233347.7.dec	2573037H1	1212	1427

Table 2 cont.

47	233347.7.dec	g3801129	1214	1602
47	233347.7.dec	g4081128	1218	1600
47	233347.7.dec	g3055817	1218	1598
47	233347.7.dec	g4242736	1229	1602
47	233347.7.d c	g4451163	1230	1602
47	233347.7.dec	g1118375	1247	1602
47	233347.7.dec	g3432030	1249	1607
47	233347.7.dec	1255671H1	1257	1496
47	233347.7.dec	3367489H1	1264	1532
47	233347.7.dec	g875829	1276	1613
47	233347.7.dec	817888H1	1284	1439
47	233347.7.dec	817819R1	1284	1597
47	233347.7.dec	817888T1	1284	1568
47	233347.7.dec	2696485H1	1287	1573
47	233347.7.dec	g1745356	1287	1597
47	233347.7.dec	g2740671	1290	1604
47	233347.7.dec	g3744937	1294	1599
47	233347.7.dec	1850503T6	1297	1550
47	233347.7.dec	g4018301	1297	1607
47	233347.7.dec	2603385H1	1301	1585
47	233347.7.dec	1751069H1	1302	1552
47	233347.7.dec	5022514H1	1304	1567
47	233347.7.dec	1712736H1	1307	1510
47	233347.7.dec	g5589583	1318	1603
47	233347.7.dec	g1441730	1327	1597
47	233347.7.dec	g1265371	1328	1597
47	233347.7.dec	g2148455	1338	1598
47	233347.7.dec	1211548T1	1343	1559
47	233347.7.dec	1211548R1	1343	1597
47	233347.7.dec	1211548H1	1343	1587
47	233347.7.dec	1211827H1	1343	1554
47	233347.7.dec	g1376380	1351	1603
47	233347.7.dec	823970H1	1361	1588
47	233347.7.dec	823970T1	1361	1567
47	233347.7.dec	2059287R6	1362	1601
47	233347.7.dec	2059287T6	1362	1560
47	233347.7.dec	2059287H1	1362	1601
47	233347.7.dec	6508958H1	1366	1602
47	233347.7.dec	3886266H1	1366	1597
47	233347.7.dec	6508772H1	1366	1597
47	233347.7.dec	6509058H1	1366	1602
47	233347.7.dec	g3229477	1368	1608
47	233347.7.dec	g1745258	1378	1601
47	233347.7.dec	g5541313	1382	1603
47	233347.7.dec	2271444H1	1385	1650
47	233347.7.dec	2596829H1	126	366
47	233347.7.dec	4575094H1	127	372
47	233347.7.dec	3488933H1	127	409
47	233347.7.dec	4029754F6	144	625
47	233347.7.dec	4670215H1	157	406
47	233347.7.dec	2132811R6	442	783
47	233347.7.dec	1864389F6	90	584
47	233347.7.dec	4533085H1	1433	1561
47	233347.7.dec	2986556H1	1434	1641
47	233347.7.dec	g3001042	1452	1557
47	233347.7.dec	g870389	1452	1611
47	233347.7.dec	716558H1	1459	1598
47	233347.7.dec	g2409880	1463	1601
47	233347.7.dec	2007017H1	1468	1589
47	233347.7.dec	g1152486	1472	1602
47	233347.7.dec	3408407H1	1503	1599
47	233347.7.dec	1429459H1	1503	1589
47	233347.7.dec	2130011H1	1550	1602
47	233347.7.dec	2530774H1	666	911
47	233347.7.dec	136644H1	689	803
47	233347.7.dec	136644R1	690	1241
47	233347.7.d c	4823525H1	697	955
47	233347.7.dec	2077355H1	159	411
47	233347.7.dec	g1087689	159	488
47	233347.7.dec	1570510H1	639	847
47	233347.7.dec	2212187H1	651	898
47	233347.7.dec	4372847H1	664	930
47	233347.7.dec	3284855H1	627	877
47	233347.7.dec	5563079H2	643	864
47	233347.7.dec	3272517H1	610	854
47	233347.7.dec	g1993674	616	902
47	233347.7.dec	1547439H1	625	818
47	233347.7.dec	3643471H1	111	372
47	233347.7.dec	2768515H1	112	371
47	233347.7.dec	3292537H1	114	357
47	233347.7.dec	3584195H1	114	407
47	233347.7.dec	5174003H1	123	293
47	233347.7.dec	552545H1	99	349
47	233347.7.dec	3376785H1	101	343
47	233347.7.dec	4528021H1	104	369
47	233347.7.dec	5587484H1	111	343
47	233347.7.dec	3140140H1	112	395
47	233347.7.dec	g3181189	1384	1599
47	233347.7.dec	1308667H1	1387	1598
47	233347.7.dec	g2279662	1395	1642
47	233347.7.dec	2233346H1	1396	1599
47	233347.7.dec	g3919171	1404	1602
47	233347.7.dec	2708745H1	1412	1596
47	233347.7.dec	1355275H1	1412	1598
47	233347.7.dec	1857353H1	1420	1529
47	233347.7.dec	1630051H1	1424	1602
47	233347.7.dec	g2464362	1430	1602
47	233347.7.dec	2088964H1	1433	1592
47	233347.7.dec	g879584	115	435
47	233347.7.dec	6180192H1	116	381
47	233347.7.dec	g4530586	115	1489
47	233347.7.dec	2734994H1	118	366
47	233347.7.dec	4062620H1	120	356
47	233347.7.dec	5322926H1	704	958
47	233347.7.dec	630038H1	723	948
47	233347.7.dec	4110187H1	739	924
47	233347.7.dec	3373756H1	735	974
47	233347.7.dec	4816662H1	92	341
47	233347.7.dec	1864389H1	90	290
47	233347.7.dec	g870430	92	392
47	233347.7.dec	2851689H1	96	342
47	233347.7.dec	256695H1	97	437
47	233347.7.dec	1222808H1	538	731
47	233347.7.dec	1428729H1	538	727
47	233347.7.dec	5422978H1	536	781
47	233347.7.dec	g2025391	538	744
47	233347.7.dec	705632H1	335	563
47	233347.7.dec	2191523H1	339	651
47	233347.7.dec	g1958225	361	762
47	233347.7.dec	2867830H1	410	716
47	233347.7.dec	1250683H1	417	614
47	233347.7.dec	2132811H1	442	702
47	233347.7.dec	782138R6	206	698
47	233347.7.dec	4318806H1	214	478
47	233347.7.dec	g1147033	216	522
47	233347.7.dec	383152H1	219	506
47	233347.7.dec	1426535H1	254	501
47	233347.7.dec	5262088H2	273	486
47	233347.7.dec	5665894H1	273	522
47	233347.7.dec	4640923H1	279	534
47	233347.7.dec	869410H1	281	533
47	233347.7.dec	869410R1	281	827
47	233347.7.dec	1683282F7	295	698
47	233347.7.dec	2681759H1	312	549
47	233347.7.dec	3950419H1	192	484
47	233347.7.dec	5671565H1	195	416

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47	233347.7.dec	g1301265	202	647	48	230631.3.dec	568183T6	1530	2106
47	233347.7.dec	782138H1	206	440	48	230631.3.dec	2611995T6	1550	2099
47	233347.7.dec	2925307H1	160	433	48	230631.3.dec	3186434H1	1585	1904
47	233347.7.dec	2572744H1	162	393	48	230631.3.dec	g2100758	1686	2142
47	233347.7.dec	2837523H2	162	401	48	230631.3.dec	g5396058	1705	2147
47	233347.7.dec	1520110H1	81	279	48	230631.3.dec	435524R6	1712	2026
47	233347.7.dec	643890H1	81	323	48	230631.3.dec	6314425H1	1	571
47	233347.7.dec	2893074H1	81	349	48	230631.3.dec	5512314F6	134	411
47	233347.7.dec	2506817F6	82	586	48	230631.3.dec	5512314H1	134	407
47	233347.7.dec	2506817H1	82	327	48	230631.3.dec	6124182H1	171	652
47	233347.7.dec	2210548H1	90	221	48	230631.3.dec	6352048H2	279	524
47	233347.7.dec	g1993764	114	386	48	230631.3.dec	5151685F6	432	780
47	233347.7.dec	4671365H1	115	382	48	230631.3.dec	5151685H1	432	697
47	233347.7.dec	5196870H1	115	305	48	230631.3.dec	g2100757	477	966
47	233347.7.dec	4671357H1	115	381	48	230631.3.dec	g1014169	477	568
47	233347.7.dec	5370648H1	111	243	48	230631.3.dec	3750444H1	494	773
47	233347.7.dec	2993361H1	1	316	48	230631.3.dec	5545516H1	750	948
47	233347.7.dec	3765582H1	36	324	48	230631.3.dec	747404H1	1112	1344
47	233347.7.dec	g2011491	108	403	48	230631.3.dec	2611995H1	1172	1415
47	233347.7.dec	3759276H1	107	412	48	230631.3.dec	6109396H1	846	1159
47	233347.7.dec	2364631H1	107	339	48	230631.3.dec	5605261H1	965	1231
47	233347.7.dec	3660890H1	111	358	48	230631.3.dec	5101319H1	1033	1301
47	233347.7.dec	2879058F6	457	839	48	230631.3.dec	568183H1	1070	1382
47	233347.7.dec	g1376379	458	816	48	230631.3.dec	568183R6	1070	1634
47	233347.7.dec	6138586H1	464	763	48	230631.3.dec	3804195H1	1086	1385
47	233347.7.dec	1930146H1	464	716	48	230631.3.dec	2759470H1	1096	1366
47	233347.7.dec	6116446H1	464	746	49	335146.1.dec	2695263F6	536	1060
47	233347.7.dec	2879058H1	456	781	49	335146.1.dec	g2719161	570	699
47	233347.7.dec	6138487H1	464	763	49	335146.1.dec	g4891403	1	447
47	233347.7.dec	3038850H1	484	769	49	335146.1.dec	g4891292	1	462
47	233347.7.dec	5292177H2	485	713	49	335146.1.dec	g4311647	1	414
47	233347.7.dec	g828019	491	831	49	335146.1.dec	g3887245	1	309
47	233347.7.dec	1850504H1	499	809	49	335146.1.dec	878550H1	247	471
47	233347.7.dec	4615174H1	506	772	49	335146.1.dec	g4266690	365	696
47	233347.7.dec	3811338H1	506	784	49	335146.1.dec	2695263H1	536	664
47	233347.7.dec	2278915H1	509	782	50	337160.1.dec	g3239640	1312	1540
47	233347.7.dec	2687896H1	511	760	50	337160.1.dec	g2080803	1319	1543
47	233347.7.dec	2595364H1	111	352	50	337160.1.dec	g4269757	1329	1533
47	233347.7.dec	3576583H1	104	410	50	337160.1.dec	g5633598	1271	1537
48	230631.3.dec	435524H1	1712	1808	50	337160.1.dec	g1421937	1279	1536
48	230631.3.dec	435524T6	1712	2104	50	337160.1.dec	5167368H1	563	803
48	230631.3.dec	g1927614	1714	2138	50	337160.1.dec	g752491	609	905
48	230631.3.dec	6410396H1	1719	2030	50	337160.1.dec	g1422034	686	1027
48	230631.3.dec	g4311787	1727	2143	50	337160.1.dec	5490664H1	696	990
48	230631.3.dec	g3214289	1738	2142	50	337160.1.dec	3749493T6	916	1491
48	230631.3.dec	g2567651	1772	2007	50	337160.1.dec	g3593694	1073	1447
48	230631.3.dec	g2901561	1772	2007	50	337160.1.dec	3749493H1	6	294
48	230631.3.dec	g5452257	1778	2147	50	337160.1.dec	g5232677	1075	1538
48	230631.3.dec	3870968H1	1783	2068	50	337160.1.dec	g1925336	11	448
48	230631.3.dec	g2898784	1802	2007	50	337160.1.dec	g5526629	1109	1538
48	230631.3.dec	g656370	1820	2163	50	337160.1.dec	g3596807	1110	1533
48	230631.3.dec	1723586T6	1844	2102	50	337160.1.dec	g2106751	105	561
48	230631.3.dec	6556178H1	1845	2142	50	337160.1.dec	5923530H1	108	394
48	230631.3.dec	6551620H1	1845	2159	50	337160.1.dec	4402877H1	135	389
48	230631.3.dec	1430637H1	1176	1437	50	337160.1.dec	g1164166	349	674
48	230631.3.dec	6558462H1	1845	2158	50	337160.1.dec	3664104H1	440	732
48	230631.3.dec	6551720H1	1845	2142	50	337160.1.dec	3457353T6	1110	1488
48	230631.3.dec	g4853053	1866	2147	50	337160.1.dec	g752492	1196	1538
48	230631.3.dec	g4688016	1866	2147	50	337160.1.dec	g4153397	1271	1537
48	230631.3.dec	g1844455	1896	2145	50	337160.1.dec	3457353F6	1	483
48	230631.3.dec	g2208492	1906	2144	50	337160.1.dec	3457353H1	1	247
48	230631.3.dec	4255443H1	1222	1473	50	337160.1.dec	3749493F6	6	343
48	230631.3.dec	2861393F6	1916	2145	51	346341.12.dec	g697197	1936	2305
48	230631.3.dec	2861393H1	1916	2145	51	346341.12.dec	g1953531	1936	2242
48	230631.3.dec	4720434H1	1922	2028	51	346341.12.dec	4549651H1	1955	2218
48	230631.3.dec	294274H1	1962	2100	51	346341.12.dec	4860447H1	2030	2109
48	230631.3.dec	5445032H1	2036	2146	51	346341.12.dec	5398105H1	2057	2333
48	230631.3.dec	5288940H1	1407	1622	51	346341.12.dec	g1952108	2153	2448

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51	346341.12.dec g4085571	2164	2580
51	346341.12.dec 2655214H1	2217	2504
51	346341.12.dec 3678964H1	2306	2470
51	346341.12.dec g1974712	2812	3086
51	346341.12.dec 461156H1	2319	2558
51	346341.12.dec 371775H1	2860	3002
51	346341.12.dec 406133H1	2418	2659
51	346341.12.dec 407852H1	2418	2654
51	346341.12.dec 4671487H1	2473	2706
51	346341.12.dec 724937H1	2497	2724
51	346341.12.dec 1850170H1	2531	2801
51	346341.12.dec 788800H1	2975	3252
51	346341.12.dec 2238012H1	2582	2836
51	346341.12.dec 788800R1	2975	3491
51	346341.12.dec 1212594H1	2619	2789
51	346341.12.dec 4110759H1	2663	2894
51	346341.12.dec 5086055H1	2744	2985
51	346341.12.dec 5034582H1	2779	3043
51	346341.12.dec 2790584H1	3072	3346
51	346341.12.dec 5034566H1	2780	3044
51	346341.12.dec 2918021H1	2791	3074
51	346341.12.dec 4548080H1	3126	3405
51	346341.12.dec 4549651T1	3136	3680
51	346341.12.dec 1251314H1	3172	3408
51	346341.12.dec 3784388H1	3183	3409
51	346341.12.dec 2767486H1	3187	3425
51	346341.12.dec 1457486H1	3201	3374
51	346341.12.dec 1457116H1	3201	3443
51	346341.12.dec 4714829H1	3207	3490
51	346341.12.dec 4522268H1	3221	3459
51	346341.12.dec 1868560H1	3241	3497
51	346341.12.dec 1870079H1	3241	3487
51	346341.12.dec 446846H1	3248	3578
51	346341.12.dec g3134178	3254	3631
51	346341.12.dec g5425839	3259	3718
51	346341.12.dec g2836424	3262	3716
51	346341.12.dec 2120370H1	3263	3512
51	346341.12.dec 2404565H1	3268	3509
51	346341.12.dec 1880015H1	3277	3542
51	346341.12.dec g3246305	3284	3716
51	346341.12.dec g5593413	3308	3717
51	346341.12.dec g3191458	3314	3717
51	346341.12.dec g5636268	3316	3716
51	346341.12.dec g4738223	3319	3716
51	346341.12.dec 3218761H1	3328	3628
51	346341.12.dec 5340713H1	3337	3539
51	346341.12.dec g3721515	3354	3716
51	346341.12.dec 5187190H1	3378	3600
51	346341.12.dec 4642347H1	3379	3646
51	346341.12.dec 1547041H1	3381	3590
51	346341.12.dec g900509	3383	3726
51	346341.12.dec g2620334	3388	3716
51	346341.12.dec g2968141	3392	3716
51	346341.12.dec g3837261	3408	3823
51	346341.12.dec g3110248	3406	3825
51	346341.12.dec g2019976	3413	3717
51	346341.12.dec g767899	3426	3718
51	346341.12.dec g698251	3451	3718
51	346341.12.dec g2695526	3478	3716
51	346341.12.dec g3756419	3517	3716
51	346341.12.dec g796770	3518	3729
51	346341.12.dec g3919176	3518	3716
51	346341.12.dec g2329740	3522	3716
51	346341.12.dec 3890462H1	3523	3612
51	346341.12.dec g2768986	3537	3716
51	346341.12.dec 062891H1	1872	2137
51	346341.12.dec 6490979H1	1880	2442
51	346341.12.dec 3314406H1	1881	2132
51	346341.12.dec 6096790H1	1892	2171
51	346341.12.dec g1983854	1914	2201
51	346341.12.dec 4602467H1	1	269
51	346341.12.dec 2944936H2	71	351
51	346341.12.dec 5686792H1	84	352
51	346341.12.dec g1985487	117	444
51	346341.12.dec 5909568H1	155	438
51	346341.12.dec 2930688H2	214	506
51	346341.12.dec 5447067H1	237	499
51	346341.12.dec 2754701H1	373	628
51	346341.12.dec 3402751H1	511	769
51	346341.12.dec 1613125H1	535	715
51	346341.12.dec 6161920H1	656	889
51	346341.12.dec 6162985H1	656	889
51	346341.12.dec 2508603H1	821	1067
51	346341.12.dec 637104H1	851	1117
51	346341.12.dec 632668H1	851	1097
51	346341.12.dec 6452454H2	1014	1468
51	346341.12.dec 5500118H1	1149	1417
51	346341.12.dec 1525276H1	1153	1384
51	346341.12.dec 967743H1	1165	1426
51	346341.12.dec 4248617H1	1166	1399
51	346341.12.dec 3333021H1	1165	1418
51	346341.12.dec 4106103H1	1184	1443
51	346341.12.dec 2135513H1	1170	1427
51	346341.12.dec 5430803H1	1181	1421
51	346341.12.dec 3287061H1	1212	1319
51	346341.12.dec 5430764H1	1230	1489
51	346341.12.dec 5953804H1	1244	1569
51	346341.12.dec 3002616H1	1251	1494
51	346341.12.dec 1793327H1	1262	1512
51	346341.12.dec 5505305H1	1268	1486
51	346341.12.dec 2159582H1	1273	1431
51	346341.12.dec g2238358	1317	1591
51	346341.12.dec 6456333H1	1365	2013
51	346341.12.dec 3161945H1	1385	1661
51	346341.12.dec 4551786H1	1409	1607
51	346341.12.dec 890596H1	1459	1730
51	346341.12.dec 899800H1	1475	1752
51	346341.12.dec g4307656	1480	1829
51	346341.12.dec 1231448H1	1494	1734
51	346341.12.dec g3336553	1499	1882
51	346341.12.dec 2991495H1	1500	1773
51	346341.12.dec 4066993H1	1517	1788
51	346341.12.dec 4801741H1	1517	1777
51	346341.12.dec 1992208H1	1528	1821
51	346341.12.dec 4958003H1	1567	1824
51	346341.12.dec 3153981H1	1573	1845
51	346341.12.dec 3280967H1	1578	1828
51	346341.12.dec 6423266H1	1581	2202
51	346341.12.dec 3758378H1	1605	1787
51	346341.12.dec 3405995H1	1587	1825
51	346341.12.dec 3000267H1	1597	1885
51	346341.12.dec 2564228H1	1599	1864
51	346341.12.dec 3000290H1	1602	1885
51	346341.12.dec 1892929H1	1604	1867
51	346341.12.dec 5085217H1	1605	1838
51	346341.12.dec g4293164	1606	1874
51	346341.12.dec 6138514H1	1634	1934
51	346341.12.dec 6138676H1	1635	1890
51	346341.12.dec 2253884H1	1618	1870
51	346341.12.dec 3340411H1	1618	1864
51	346341.12.dec 3792137H1	1620	1925
51	346341.12.dec 4240984H1	1622	1986
51	346341.12.dec 1218145H1	1624	1872
51	346341.12.dec 5079596H1	1630	1853
51	346341.12.dec 3859531H1	1630	1871
51	346341.12.dec 6141523H1	1630	1890

Table 2 cont.

51	346341.12.dec	3039280H1	1630	1914
51	346341.12.dec	2579416H1	1630	1872
51	346341.12.dec	g2589524	1634	1874
51	346341.12.dec	2553812H1	1634	1884
51	346341.12.dec	2834664H1	1644	1895
51	346341.12.dec	4061342H1	1644	1822
51	346341.12.dec	4941567H1	1648	1916
51	346341.12.dec	1711165H1	1665	1863
51	346341.12.dec	4123360H1	1719	1878
51	346341.12.dec	2964132H1	1746	1916
51	346341.12.dec	4252513H1	1735	1896
51	346341.12.dec	1998609H1	1736	1872
51	346341.12.dec	4543814H1	1754	1860
51	346341.12.dec	4111257H1	1759	2011
51	346341.12.dec	3239986H1	1847	2096
51	346341.12.dec	063028H1	1872	2078
51	346341.12.dec	064031H1	1872	2102
52	428745.2.dec	g2820616	193	532
52	428745.2.dec	g2881239	230	653
52	428745.2.dec	g1063734	241	491
52	428745.2.dec	g954024	275	581
52	428745.2.dec	6490302H1	322	915
52	428745.2.dec	724811R6	436	916
52	428745.2.dec	2562118H1	516	777
52	428745.2.dec	5463505H1	669	858
52	428745.2.dec	918149H1	1	229
52	428745.2.dec	g1991232	22	303
52	428745.2.dec	g2028636	116	368
52	428745.2.dec	5086711H1	124	374
52	428745.2.dec	5086711F6	124	666
52	428745.2.dec	g1578109	138	560
52	428745.2.dec	g1812416	142	598
52	428745.2.dec	1713552H1	181	426
52	428745.2.dec	g2881535	186	328
52	428745.2.dec	3630275H1	704	849
52	428745.2.dec	4838210H1	706	832
52	428745.2.dec	5078612H1	726	983
52	428745.2.dec	4130312H1	753	1014
52	428745.2.dec	2768676H1	767	1006
52	428745.2.dec	3448885H1	780	1025
52	428745.2.dec	4381065H1	805	1060
52	428745.2.dec	1294626T6	929	1385
52	428745.2.dec	1294626H1	936	1146
52	428745.2.dec	1294626F6	936	1423
52	428745.2.dec	1292590H1	936	1140
52	428745.2.dec	5099834H1	963	1141
52	428745.2.dec	2729359H1	1041	1228
52	428745.2.dec	2792430H1	1075	1382
52	428745.2.dec	1888850H1	1111	1387
52	428745.2.dec	6547071H1	1155	1391
53	444839.17.dec	6457190H1	1	507
53	444839.17.dec	104107H1	221	428
53	444839.17.dec	2938414H1	310	585
53	444839.17.dec	5618181R8	552	908
53	444839.17.dec	611217T6	614	805
53	444839.17.dec	611217H1	626	855
53	444839.17.dec	611217R6	626	855
54	245000.6.dec	409677H1	383	640
54	245000.6.dec	1929331H1	519	751
54	245000.6.dec	1751338H1	521	722
54	245000.6.dec	2515886H1	424	739
54	245000.6.dec	2326214H1	534	780
54	245000.6.dec	280952R6	517	959
54	245000.6.d c	2658307H1	579	822
54	245000.6.dec	3107867H1	27	299
54	245000.6.dec	3114192H1	32	298
54	245000.6.dec	3210893H1	37	105
54	245000.6.dec	860506H1	40	312
54	245000.6.dec	1355155H1	23	281
54	245000.6.dec	860506R1	40	612
54	245000.6.dec	3189465H1	44	394
54	245000.6.dec	3766993H1	25	314
54	245000.6.dec	1473691H1	50	301
54	245000.6.dec	4331373H1	50	292
54	245000.6.dec	1471541H1	50	263
54	245000.6.dec	6195212H1	50	123
54	245000.6.dec	3106926H1	27	305
54	245000.6.dec	2099640H1	50	278
54	245000.6.dec	3670326H1	57	341
54	245000.6.dec	853792H1	1	245
54	245000.6.dec	2512562H1	12	348
54	245000.6.dec	2850207H1	23	319
54	245000.6.dec	3452542H1	22	260
54	245000.6.dec	1355155F1	23	460
54	245000.6.dec	4539474H1	59	331
54	245000.6.dec	2563931H1	57	330
54	245000.6.dec	3085485H1	58	315
54	245000.6.dec	3926193H1	59	342
54	245000.6.dec	2460549H1	60	309
54	245000.6.dec	3037582H1	59	245
54	245000.6.dec	g1377709	58	403
54	245000.6.dec	3254001H1	60	321
54	245000.6.dec	2691264H1	60	318
54	245000.6.dec	4669568H1	60	327
54	245000.6.dec	2514525H1	62	392
54	245000.6.dec	2209841H1	62	310
54	245000.6.dec	851811H1	62	327
54	245000.6.dec	4599225H1	61	349
54	245000.6.dec	1286024H1	66	318
54	245000.6.dec	5075587H1	67	337
54	245000.6.dec	2515049H1	67	372
54	245000.6.dec	5530160H1	67	335
54	245000.6.dec	g1088112	73	355
54	245000.6.dec	2098876H1	75	338
54	245000.6.dec	1227790H1	76	349
54	245000.6.dec	763189H1	77	298
54	245000.6.dec	979662H1	79	372
54	245000.6.dec	2913785H1	81	346
54	245000.6.dec	2913737H1	81	338
54	245000.6.dec	3686742H1	82	375
54	245000.6.dec	4202894H1	98	208
54	245000.6.dec	2735065H1	102	318
54	245000.6.dec	3697890H1	102	367
54	245000.6.dec	2314724H1	105	333
54	245000.6.dec	2912582H1	124	391
54	245000.6.dec	139138H1	126	262
54	245000.6.dec	g1947635	124	336
54	245000.6.dec	1795035H1	137	423
54	245000.6.dec	5882992H1	149	419
54	245000.6.dec	2438787H1	148	333
54	245000.6.dec	5888569H1	149	330
54	245000.6.dec	5889878H1	150	404
54	245000.6.dec	2439472H1	150	392
54	245000.6.dec	280152H1	624	950
54	245000.6.dec	2311893H1	663	902
54	245000.6.dec	983601T1	685	1156
54	245000.6.dec	983601H1	685	971
54	245000.6.dec	346874T6	715	1156
54	245000.6.dec	280952T6	747	1126
54	245000.6.dec	694271H1	159	408
54	245000.6.dec	2413665H1	159	379
54	245000.6.dec	g1087215	184	452
54	245000.6.d c	g1799013	185	648
54	245000.6.dec	4050305H1	196	492
54	245000.6.dec	4052675H1	196	463
54	245000.6.dec	3534417H1	904	1031

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54	245000.6.dec	5328522H1	770	1038
54	245000.6.dec	g3923886	809	1193
54	245000.6.dec	3841719H1	225	472
54	245000.6.dec	3820119H1	225	509
54	245000.6.d c	4144664H1	293	580
54	245000.6.dec	3689241H1	306	575
54	245000.6.dec	2413743H1	308	445
54	245000.6.dec	5072965H2	371	636
54	245000.6.dec	1342754H1	754	983
54	245000.6.dec	3840055H1	749	1026
55	428362.36.dec	3230456H1	28	202
55	428362.36.dec	746804H1	26	250
55	428362.36.dec	4158870H1	28	294
55	428362.36.dec	871508R6	490	896
55	428362.36.dec	g4088720	500	906
55	428362.36.dec	g4110002	502	832
55	428362.36.dec	g2555797	529	900
55	428362.36.dec	g888696	531	845
55	428362.36.dec	3141069H2	557	805
55	428362.36.dec	g3240896	569	904
55	428362.36.dec	g1501350	578	879
55	428362.36.dec	g4148815	803	890
55	428362.36.dec	2500865H1	20	270
55	428362.36.dec	3136845H1	22	280
55	428362.36.dec	3616233F6	23	517
55	428362.36.dec	3616233H1	23	327
55	428362.36.dec	6420559H1	26	526
55	428362.36.dec	1949076H1	1	166
55	428362.36.dec	182957H1	19	81
55	428362.36.dec	g4074435	665	902
55	428362.36.dec	g1477032	685	905
55	428362.36.dec	g1493079	687	908
55	428362.36.dec	g4330971	690	901
55	428362.36.dec	4365938H1	695	901
55	428362.36.dec	g4510083	736	901
55	428362.36.dec	6400671H1	757	904
55	428362.36.dec	g2782804	766	906
55	428362.36.dec	1740312H1	767	907
55	428362.36.dec	g1920531	784	907
55	428362.36.dec	g3429969	793	908
55	428362.36.dec	g3093231	586	901
55	428362.36.dec	g5035307	589	896
55	428362.36.dec	g2341502	642	902
55	428362.36.dec	g1721969	643	908
55	428362.36.dec	g2177837	651	890
55	428362.36.dec	2541141T6	412	888
55	428362.36.dec	5570638H1	414	682
55	428362.36.dec	3489039H1	29	292
55	428362.36.dec	777429H1	30	169
55	428362.36.dec	6168112H1	30	526
55	428362.36.dec	5865533H1	30	313
55	428362.36.dec	3354446H1	32	303
55	428362.36.dec	3234544H1	33	270
55	428362.36.dec	g1501349	37	416
55	428362.36.dec	2571111H1	419	667
55	428362.36.dec	g2437317	426	901
55	428362.36.dec	5294742H1	450	695
55	428362.36.dec	g4687987	452	901
55	428362.36.dec	g5361739	453	901
55	428362.36.dec	g1526406	461	907
55	428362.36.dec	g4524922	478	902
55	428362.36.dec	g2933287	479	901
55	428362.36.dec	g2912603	483	910
55	428362.36.dec	044024H1	487	780
55	428362.36.dec	871508R1	489	902
55	428362.36.dec	871508H1	489	726
55	428362.36.dec	871508T6	489	864
55	428362.36.dec	g2537776	116	610
55	428362.36.dec	g1493078	129	321
55	428362.36.dec	g1721693	130	463
55	428362.36.dec	g1492722	131	551
55	428362.36.dec	4982415H1	11	290
55	428362.36.dec	2275381H1	14	258
55	428362.36.dec	g4929742	16	908
55	428362.36.dec	3400712H1	16	215
55	428362.36.dec	g1957477	16	419
55	428362.36.dec	1423179H1	17	222
55	428362.36.dec	4895906H1	20	326
55	428362.36.dec	546870H1	20	267
55	428362.36.dec	g4329321	242	670
55	428362.36.dec	1823626T6	255	858
55	428362.36.dec	g1635280	296	683
55	428362.36.dec	4746558H1	325	564
55	428362.36.dec	g2178537	333	539
55	428362.36.dec	4973919H1	335	609
55	428362.36.dec	g2159511	46	394
55	428362.36.dec	1998274H1	48	119
55	428362.36.dec	2413133H1	48	270
55	428362.36.dec	833838H1	52	335
55	428362.36.dec	1467759H1	48	244
55	428362.36.dec	6111241H1	52	336
55	428362.36.dec	835269H1	52	323
55	428362.36.dec	4508403H1	38	303
55	428362.36.dec	5309028H1	40	301
55	428362.36.dec	4352115H1	42	292
55	428362.36.dec	2661812H1	45	314
55	428362.36.dec	3616233T6	347	875
55	428362.36.dec	1470246H1	365	553
55	428362.36.dec	2588112F6	372	681
55	428362.36.dec	2588112H1	372	632
55	428362.36.dec	2588112T6	373	632
55	428362.36.dec	g2987835	405	834
55	428362.36.dec	4550658T1	410	861
55	428362.36.dec	475963H1	186	448
55	428362.36.dec	4337255H1	194	456
55	428362.36.dec	4071782H1	131	398
55	428362.36.dec	6125624H1	155	627
55	428362.36.dec	460302H1	212	473
55	428362.36.dec	5853923H1	162	426
55	428362.36.dec	4914457H1	174	417
55	428362.36.dec	4871852H1	1	278
55	428362.36.dec	5517108H1	6	280
55	428362.36.dec	4420778H1	8	268
55	428362.36.dec	5043882H1	11	278
55	428362.36.dec	6119524H1	12	622
55	428362.36.dec	711540H1	65	340
55	428362.36.dec	5482919H1	68	347
55	428362.36.dec	716182H1	69	281
55	428362.36.dec	4922936H1	71	339
55	428362.36.dec	3234867H1	71	315
55	428362.36.dec	4981082H1	75	356
55	428362.36.dec	5029845H1	97	333
55	428362.36.dec	2490005H1	108	346
55	428362.36.dec	1320555H1	52	300
55	428362.36.dec	4550658H1	52	296
55	428362.36.dec	4798082H1	53	287
55	428362.36.dec	g2161592	53	489
56	480710.12.dec	g5235305	4035	4473
56	480710.12.dec	g1557590	4036	4470
56	480710.12.dec	880717T1	4038	4430
56	480710.12.dec	880717R1	4038	4330
56	480710.12.dec	880717H1	4038	4275
56	480710.12.dec	g4084804	4044	4473
56	480710.12.dec	4371905H1	4050	4314
56	480710.12.dec	4506862H1	4057	4317
56	480710.12.dec	g2541764	4059	4474

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56	480710.12.dec g5367783	4060	4470	56	480710.12.dec 1215902H1	3570	3798
56	480710.12.dec g678587	4067	4441	56	480710.12.dec 1657958H1	3571	3779
56	480710.12.dec g4607015	4071	4475	56	480710.12.dec g2229755	3550	4000
56	480710.12.dec g4535236	4071	4470	56	480710.12.dec 310435H1	3564	3761
56	480710.12.dec 2900362H1	4081	4354	56	480710.12.dec 4885652H1	3545	3749
56	480710.12.dec g918370	4081	4391	56	480710.12.dec 2874149H1	3715	3988
56	480710.12.dec 3836936H1	4091	4374	56	480710.12.dec 3444009H1	3729	3987
56	480710.12.dec g1692010	4092	4484	56	480710.12.dec 782063R1	3906	4445
56	480710.12.dec 1334882H1	4119	4351	56	480710.12.dec g5636497	3210	3491
56	480710.12.dec 4861120H1	4119	4386	56	480710.12.dec 4740585H2	3218	3486
56	480710.12.dec 1351565F1	4125	4470	56	480710.12.dec 3453705H1	3219	3337
56	480710.12.dec 1351565H1	4125	4376	56	480710.12.dec 4350876H1	3225	3357
56	480710.12.dec 1351565F6	4125	4474	56	480710.12.dec g2059287	3177	3489
56	480710.12.dec 1377778T6	4126	4441	56	480710.12.dec g727073	3173	3464
56	480710.12.dec g3108603	4131	4475	56	480710.12.dec 554290R6	3343	3839
56	480710.12.dec 2271108H1	4132	4395	56	480710.12.dec 554290H1	3343	3563
56	480710.12.dec 2271114H1	4132	4390	56	480710.12.dec g2775291	3346	3486
56	480710.12.dec 4954215H1	4134	4389	56	480710.12.dec 5298647H1	3350	3594
56	480710.12.dec 5599026H1	4134	4378	56	480710.12.dec 3172587H1	3357	3631
56	480710.12.dec g4299288	4141	4445	56	480710.12.dec 2041156H1	3360	3625
56	480710.12.dec g813687	4143	4480	56	480710.12.dec 2766832F6	3378	3780
56	480710.12.dec g4524478	4154	4470	56	480710.12.dec 2766840H1	3378	3604
56	480710.12.dec g1266072	4169	4470	56	480710.12.dec 3270815H1	3707	3959
56	480710.12.dec g768815	4173	4472	56	480710.12.dec 5189122H1	3714	3932
56	480710.12.dec g958680	4174	4438	56	480710.12.dec 3072628H1	3285	3577
56	480710.12.dec 5104025H1	4188	4445	56	480710.12.dec 4700004H1	1600	1879
56	480710.12.dec g657133	4194	4473	56	480710.12.dec 1711787H1	1664	1877
56	480710.12.dec g715881	4195	4474	56	480710.12.dec g2031416	1698	1952
56	480710.12.dec g1748430	4200	4471	56	480710.12.dec 6485042H1	1723	2292
56	480710.12.dec g2556567	4213	4478	56	480710.12.dec 4989752H1	1726	1847
56	480710.12.dec g656966	4214	4470	56	480710.12.dec 4989774H1	1725	1963
56	480710.12.dec 4199390H1	4230	4472	56	480710.12.dec g1087373	1742	2115
56	480710.12.dec 4110342H1	4260	4405	56	480710.12.dec 130838R6	1747	2258
56	480710.12.dec g1025062	4265	4433	56	480710.12.dec 130838H1	1746	1928
56	480710.12.dec 598848H1	4270	4470	56	480710.12.dec g1271319	1768	2109
56	480710.12.dec 4825131H1	3886	4138	56	480710.12.dec 3291281H1	1802	1927
56	480710.12.dec 2361847T6	3888	4433	56	480710.12.dec 3692084H1	1821	2099
56	480710.12.dec 374196H1	3488	3728	56	480710.12.dec 3400646H1	1877	2103
56	480710.12.dec 2462560H1	3801	4047	56	480710.12.dec g1471362	1885	2122
56	480710.12.dec 4590905H1	3787	4017	56	480710.12.dec 3522564H1	1902	2212
56	480710.12.dec g2264982	4237	4473	56	480710.12.dec g5394524	3039	3486
56	480710.12.dec g2266184	4243	4467	56	480710.12.dec g5394523	3040	3486
56	480710.12.dec g5638968	4244	4470	56	480710.12.dec g3431663	3042	3494
56	480710.12.dec g5594372	4247	4470	56	480710.12.dec 3801488H1	3255	3509
56	480710.12.dec g1443422	4250	4470	56	480710.12.dec 2798884H1	3265	3509
56	480710.12.dec g761095	4252	4446	56	480710.12.dec g1636310	3271	3454
56	480710.12.dec 3118128H1	4257	4470	56	480710.12.dec g2694542	3040	3487
56	480710.12.dec 5436689H1	3403	3598	56	480710.12.dec g1358669	3058	3486
56	480710.12.dec 5487134H1	3431	3682	56	480710.12.dec g1025257	4297	4441
56	480710.12.dec 5284219H1	3504	3657	56	480710.12.dec g1748444	4305	4471
56	480710.12.dec 2099792H1	3541	3699	56	480710.12.dec g5438233	4383	4474
56	480710.12.dec g922955	3308	3487	56	480710.12.dec 5064281H1	1910	2138
56	480710.12.dec 3614786H1	3316	3614	56	480710.12.dec g1690244	1919	2165
56	480710.12.dec 6389577H1	3321	3566	56	480710.12.dec 4539338H1	1945	2181
56	480710.12.dec g1920533	3321	3486	56	480710.12.dec 4540969H1	1945	2196
56	480710.12.dec g958726	3616	3861	56	480710.12.dec 3377229H1	2045	2296
56	480710.12.dec 5495496R6	3618	3943	56	480710.12.dec 2657748F6	2113	2548
56	480710.12.dec 884462H1	3629	3864	56	480710.12.dec 2657748H1	2113	2327
56	480710.12.dec g715880	3615	3900	56	480710.12.dec 4302139H1	2278	2555
56	480710.12.dec 5037750H1	3632	3867	56	480710.12.dec 190789R6	2288	2700
56	480710.12.dec 3478382H1	3651	3845	56	480710.12.dec 190789H1	2289	2455
56	480710.12.dec 390082H1	3655	3933	56	480710.12.dec 2971888H2	2297	2573
56	480710.12.dec 1845386R6	3669	4009	56	480710.12.dec 3050381H1	2321	2600
56	480710.12.dec g4149091	3300	3464	56	480710.12.dec 1363666F6	2341	2843
56	480710.12.dec g5233011	3302	3486	56	480710.12.dec 1363666H1	2341	2550
56	480710.12.dec 3220964H1	3303	3633	56	480710.12.dec 2379137H1	2373	2594
56	480710.12.dec g919138	3315	3635	56	480710.12.dec 3254033H1	2390	2628
56	480710.12.dec 6552777H1	3570	4095	56	480710.12.dec 5056123H1	2399	2673

Table 2 cont.

56	480710.12.dec g1968577	2420	2694
56	480710.12.dec 3450783H1	2443	2689
56	480710.12.dec 427384H1	2501	2606
56	480710.12.dec 4358866H1	2568	2831
56	480710.12.dec 6549881H1	2604	3093
56	480710.12.dec 1444544H1	2637	2908
56	480710.12.dec g1358409	2736	3179
56	480710.12.dec 1436708F1	2737	3258
56	480710.12.dec 1436708H1	2737	3006
56	480710.12.dec 1438425H1	2737	2979
56	480710.12.dec 1627631F6	2757	3064
56	480710.12.dec 1627631H1	2757	2951
56	480710.12.dec 197491H1	2785	2977
56	480710.12.dec 2830313H1	2798	3035
56	480710.12.dec g1383816	2839	3174
56	480710.12.dec 4319982H1	2847	3123
56	480710.12.dec 494817T7	2899	3448
56	480710.12.dec 2070657H1	2904	3179
56	480710.12.dec 751662H1	2923	3156
56	480710.12.dec 1911471F6	2925	3484
56	480710.12.dec 1911471H1	2925	3200
56	480710.12.dec 4254047H1	2933	3208
56	480710.12.dec 2234211T6	2941	3468
56	480710.12.dec 494817T6	2943	3449
56	480710.12.dec 2797596F6	2948	3425
56	480710.12.dec 3175668H1	3228	3316
56	480710.12.dec g2218996	3230	3464
56	480710.12.dec g1030553	3235	3488
56	480710.12.dec g1690139	3241	3486
56	480710.12.dec 554290T6	3954	4429
56	480710.12.dec 2766832T6	3971	4425
56	480710.12.dec 2654374H1	4000	4295
56	480710.12.dec 1627631T6	4005	4429
56	480710.12.dec g4451104	4005	4471
56	480710.12.dec 2415120H1	3783	4029
56	480710.12.dec 2414680H1	3783	4012
56	480710.12.dec 1545383H1	3489	3684
56	480710.12.dec 4043654H1	3497	3769
56	480710.12.dec 1845386H1	3669	3952
56	480710.12.dec g761231	3669	3974
56	480710.12.dec g761199	3669	3804
56	480710.12.dec g1747939	3685	3988
56	480710.12.dec g1747953	3685	3770
56	480710.12.dec 343669H1	3703	3926
56	480710.12.dec g5446447	4008	4470
56	480710.12.dec g4084680	4013	4473
56	480710.12.dec g4395415	4014	4471
56	480710.12.dec 3477237H1	3732	4051
56	480710.12.dec 5059174H1	3744	4010
56	480710.12.dec g1509756	3770	3926
56	480710.12.dec 6305758H1	3771	4333
56	480710.12.dec 6560135H1	3896	4442
56	480710.12.dec 5710595H2	3897	4139
56	480710.12.dec 1795278H1	3842	4079
56	480710.12.dec 1795278R6	3842	4079
56	480710.12.dec 628002H1	3845	4108
56	480710.12.dec g680620	3859	4074
56	480710.12.dec 1944608H1	3807	4077
56	480710.12.dec g1320173	3819	4027
56	480710.12.dec 5487143H1	3590	3865
56	480710.12.dec 4905295H1	3591	3852
56	480710.12.dec 1840923R6	3613	4077
56	480710.12.dec g1973746	3613	3912
56	480710.12.dec g1025256	3616	3900
56	480710.12.dec 1995310R6	3501	3878
56	480710.12.dec 1995310H1	3501	3760
56	480710.12.dec 5584069H1	3504	3732
56	480710.12.dec 782063H1	3906	4120
56	480710.12.dec 2732286H1	3906	4120
56	480710.12.dec 465744H1	3945	4176
56	480710.12.dec 1840923T6	3948	4432
56	480710.12.dec 2722361T6	3953	4443
56	480710.12.dec 2722361H1	34	293
56	480710.12.dec 6482171H1	155	615
56	480710.12.dec g2219055	236	491
56	480710.12.dec g4327833	345	695
56	480710.12.dec g1985324	386	601
56	480710.12.dec 4677757H1	402	671
56	480710.12.dec 3592515H1	429	742
56	480710.12.dec 3322162F6	469	987
56	480710.12.dec 3322162H1	469	751
56	480710.12.dec 3281467H1	505	759
56	480710.12.dec 3281459H1	505	656
56	480710.12.dec 3824991H1	588	863
56	480710.12.dec 574866H1	595	823
56	480710.12.dec 4186145H1	798	1131
56	480710.12.dec 3373301H1	849	1100
56	480710.12.dec 2968518H1	948	1257
56	480710.12.dec 6378908H1	978	1160
56	480710.12.dec 494817R6	1099	1499
56	480710.12.dec 494817R7	1099	1316
56	480710.12.dec 4158239H1	1179	1426
56	480710.12.dec 5218041H1	1363	1621
56	480710.12.dec g1406348	1408	1833
56	480710.12.dec g1447767	1409	1834
56	480710.12.dec 3763147H1	1435	1636
56	480710.12.dec 2361847R6	1440	1727
56	480710.12.dec 2361847H1	1440	1685
56	480710.12.dec 6382348H1	1458	1539
56	480710.12.dec 2780247H1	1509	1743
56	480710.12.dec 5330032H1	1541	1807
56	480710.12.dec 1345161H1	1579	1813
56	480710.12.dec g922956	4297	4475
56	480710.12.dec g751917	3166	3478
56	480710.12.dec g3801141	3094	3492
56	480710.12.dec g5395425	3100	3486
56	480710.12.dec 5297004H1	3106	3357
56	480710.12.dec 5296912H1	3106	3336
56	480710.12.dec g5671278	3114	3488
56	480710.12.dec g3231367	3139	3493
56	480710.12.dec g2619569	3148	3507
56	480710.12.dec 4117814H1	3156	3428
56	480710.12.dec 4114196H1	3156	3420
56	480710.12.dec g1194833	3156	3486
56	480710.12.dec g1383757	3160	3486
56	480710.12.dec g3239398	3161	3486
56	480710.12.dec g4222799	3055	3486
56	480710.12.dec g1994805	3060	3486
56	480710.12.dec g3278265	3060	3490
56	480710.12.dec g4076954	3079	3485
56	480710.12.dec 1363666T6	3084	3439
56	480710.12.dec g2743581	3085	3489
56	480710.12.dec g761125	4287	4463
56	480710.12.dec 4940537H1	4292	4445
56	480710.12.dec 598928H1	4270	4383
56	480710.12.dec 3322162T6	3873	4423
56	480710.12.dec 1995310T6	3873	4431
56	480710.12.dec 1845386T6	3874	4433
56	480710.12.dec 6407714H1	3864	4128
56	480710.12.dec 4793718H1	3865	4134
56	480710.12.dec 2433207H1	1	229
56	480710.12.dec 3082718H1	1	298
56	480710.12.dec 3589555H1	23	284
56	480710.12.dec 5644719H1	28	259
56	480710.12.dec 3613921H1	28	275
56	480710.12.dec 3147763H1	30	289

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56	480710.12.dec 2722361F6	34	544	57	234137.10.dec 6407056H1	1391	1562
56	480710.12.dec 2797596H1	2948	3197	57	234137.10.dec g2964089	1397	1563
56	480710.12.dec 3729452H1	3016	3311	57	234137.10.dec g649064	1411	1567
56	480710.12.dec 4986129H1	3018	3298	57	234137.10.dec g1264136	1380	1568
56	480710.12.dec 5451222H1	3027	3288	57	234137.10.dec g674420	1382	1484
56	480710.12.dec 5451783H1	3026	3227	57	234137.10.dec 2110777T6	1054	1541
56	480710.12.dec g3736306	3037	3490	57	234137.10.dec 535718H1	1063	1274
56	480710.12.dec 2797596T6	3038	3447	57	234137.10.dec 1440773R1	1072	1560
57	234137.10.dec g5636768	1332	1560	57	234137.10.dec 3813579H1	855	1143
57	234137.10.dec g3873139	1336	1569	57	234137.10.dec 4937088H1	870	1121
57	234137.10.dec g830941	1337	1570	57	234137.10.dec 1993760H1	154	367
57	234137.10.dec g678033	1328	1560	57	234137.10.dec 3506477H1	154	440
57	234137.10.dec g3764879	1332	1565	57	234137.10.dec g991858	160	319
57	234137.10.dec 567963H1	724	978	57	234137.10.dec g4152671	207	561
57	234137.10.dec 643036H1	753	991	57	234137.10.dec g4737226	1154	1560
57	234137.10.dec g3434330	1204	1565	57	234137.10.dec 1516507T6	1140	1526
57	234137.10.dec g4568341	1206	1561	57	234137.10.dec g4224234	1157	1567
57	234137.10.dec g4394560	1219	1560	57	234137.10.dec 1255603T6	1172	1524
57	234137.10.dec 3150617H1	717	988	57	234137.10.dec g3096244	1181	1473
57	234137.10.dec 1440773T6	1141	1520	57	234137.10.dec 3424013H1	1000	1268
57	234137.10.dec g2138832	1142	1563	57	234137.10.dec 1742695H1	1002	1207
57	234137.10.dec 3746685H1	47	317	57	234137.10.dec g3336428	1187	1565
57	234137.10.dec 6265607H1	93	216	57	234137.10.dec g3231388	1189	1560
57	234137.10.dec 2503636H1	97	332	57	234137.10.dec 1575462T6	1191	1520
57	234137.10.dec 698952H1	114	199	57	234137.10.dec 2585733H1	643	887
57	234137.10.dec.699726H1	114	366	57	234137.10.dec 1440773H1	645	908
57	234137.10.dec 699737H1	114	362	57	234137.10.dec g4075131	1202	1560
57	234137.10.dec 3051736H1	1008	1301	57	234137.10.dec 3503321H1	1200	1506
57	234137.10.dec 3789688H1	1025	1238	57	234137.10.dec g678032	1248	1560
57	234137.10.dec 389357H1	1031	1178	57	234137.10.dec 454365H1	1248	1428
57	234137.10.dec 2653885T6	1030	1522	57	234137.10.dec 3121619H1	1253	1545
57	234137.10.dec 389357R1	1034	1455	57	234137.10.dec 2867481H1	548	852
57	234137.10.dec 389357R6	1034	1426	57	234137.10.dec 3804490H1	551	852
57	234137.10.dec 4000387H1	1047	1317	57	234137.10.dec 5269079H2	559	779
57	234137.10.dec 1446567T6	1049	1521	57	234137.10.dec 5586156H1	563	725
57	234137.10.dec 4000387R6	1047	1422	57	234137.10.dec 4711212H1	564	817
57	234137.10.dec 4000387T6	1048	1526	57	234137.10.dec 3165089H1	566	832
57	234137.10.dec g2932747	1119	1560	57	234137.10.dec 3925365H1	677	960
57	234137.10.dec g4149909	1129	1566	57	234137.10.dec 5900267H1	666	950
57	234137.10.dec g3678702	1133	1563	57	234137.10.dec 5066375H1	690	941
57	234137.10.dec g2322637	1141	1560	57	234137.10.dec 5204570H1	708	961
57	234137.10.dec 644000H1	595	862	57	234137.10.dec 6111563H1	708	1024
57	234137.10.dec 4637553H1	573	818	57	234137.10.dec 3867362H1	706	960
57	234137.10.dec 3766620H1	627	862	57	234137.10.dec 1440773F6	645	1003
57	234137.10.dec 1742623H1	1002	1271	57	234137.10.dec 2736033H1	645	887
57	234137.10.dec 1742603H1	1002	1278	57	234137.10.dec 2948070H1	659	927
57	234137.10.dec 1742570H1	1002	1286	57	234137.10.dec 3872678H1	664	952
57	234137.10.dec g1004759	1003	1262	57	234137.10.dec 1482169H1	22	287
57	234137.10.dec 3124271H1	628	935	57	234137.10.dec 1602692H1	23	223
57	234137.10.dec 993448H1	632	867	57	234137.10.dec g775373	24	309
57	234137.10.dec 3875672H1	639	928	57	234137.10.dec 3530615H1	1	283
57	234137.10.dec g1813123	1485	1563	57	234137.10.dec 4171108H1	1	279
57	234137.10.dec g2631629	1507	1560	57	234137.10.dec 3156905H1	1	163
57	234137.10.dec 4077622H1	18	292	57	234137.10.dec g3191632	808	1227
57	234137.10.dec 3672287H1	17	227	57	234137.10.dec 2129471H1	807	1082
57	234137.10.dec 905762H1	20	222	57	234137.10.dec 3517838H1	819	1133
57	234137.10.dec g953765	20	379	57	234137.10.dec 5081676H1	841	1007
57	234137.10.dec 2816025H1	21	319	57	234137.10.dec 3870236H1	846	1114
57	234137.10.dec g1815065	4	440	57	234137.10.dec g3896087	1375	1560
57	234137.10.dec g884950	8	411	57	234137.10.dec g5638159	1374	1566
57	234137.10.dec 3331405H1	13	269	57	234137.10.dec 589607H1	958	1206
57	234137.10.dec 6408514H1	16	601	57	234137.10.dec 1446567H1	968	1143
57	234137.10.dec 901600H1	430	735	57	234137.10.dec 1446567F6	968	1362
57	234137.10.dec 901500R1	430	955	57	234137.10.dec g1496263	983	1304
57	234137.10.dec 901744H1	430	628	57	234137.10.dec 1832689T6	986	1522
57	234137.10.dec 5591962H1	449	578	57	234137.10.dec 2287212H1	999	1230
57	234137.10.dec 2653885H1	511	789	57	234137.10.dec 5190833H2	125	366
57	234137.10.dec g868790	1436	1571	57	234137.10.dec 2723787H1	123	373

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57	234137.10.dec 4880881H1	127	330
57	234137.10.dec 6245793H1	135	660
57	234137.10.dec 2419654H1	153	389
57	234137.10.dec 2121623F6	1100	1566
57	234137.10.dec g4763998	1106	1568
57	234137.10.dec g2875766	1115	1508
57	234137.10.dec g4985803	1120	1566
57	234137.10.dec 3327435H1	208	461
57	234137.10.dec 1832689H1	235	502
57	234137.10.dec 1832689R6	235	564
57	234137.10.dec 1711521H1	239	438
57	234137.10.dec 3317846H1	300	546
57	234137.10.dec g1616066	332	598
57	234137.10.dec 2185641H1	347	605
57	234137.10.dec 1618067H1	387	599
57	234137.10.dec g2141035	23	441
57	234137.10.dec g616022	25	291
57	234137.10.dec g705506	26	316
57	234137.10.dec g705505	26	285
57	234137.10.dec 4159960H1	26	277
57	234137.10.dec g831177	30	382
57	234137.10.dec g574383	29	350
57	234137.10.dec g868789	30	312
57	234137.10.dec g390441	30	330
57	234137.10.dec g1516946	32	435
57	234137.10.dec 1602692F6	23	311
57	234137.10.dec 2888320H1	34	305
57	234137.10.dec 2888507H1	34	96
57	234137.10.dec g814646	34	314
57	234137.10.dec 3243071H1	34	273
57	234137.10.dec 3511080H1	38	329
57	234137.10.dec 4518458H1	872	1113
57	234137.10.dec 6496453H1	885	1320
57	234137.10.dec 4344079H1	906	1194
57	234137.10.dec 4230253H1	911	1192
57	234137.10.dec g4152672	953	1290
57	234137.10.dec 5518712H1	409	640
57	234137.10.dec 1255603H1	410	653
57	234137.10.dec 1255603F6	410	762
57	234137.10.dec 901500H1	430	720
57	234137.10.dec g681938	1304	1560
57	234137.10.dec g3701283	1304	1569
57	234137.10.dec g2107226	1313	1560
57	234137.10.dec 2691496T6	1313	1534
57	234137.10.dec g814596	1323	1575
57	234137.10.dec g2782755	1324	1508
57	234137.10.dec g4327424	1282	1575
57	234137.10.dec g1516847	1289	1579
57	234137.10.dec g884865	1295	1574
57	234137.10.dec g831967	1295	1576
57	234137.10.dec g2874899	1299	1525
57	234137.10.dec g1496154	1299	1560
57	234137.10.dec g3883995	1303	1569
57	234137.10.dec 4772565H1	1258	1527
57	234137.10.dec g822266	1282	1569
57	234137.10.dec g5454513	1279	1560
57	234137.10.dec g2716433	1274	1560
57	234137.10.dec g5452927	1371	1563
57	234137.10.dec 2121623H1	1337	1566
57	234137.10.dec g4330579	1338	1566
57	234137.10.dec g4533890	1338	1560
57	234137.10.dec g566649	1347	1560
57	234137.10.dec g2752755	1348	1566
57	234137.10.dec g3424229	1373	1566
57	234137.10.dec 1964266H1	1221	1426
57	234137.10.dec 1964266R6	1221	1535
57	234137.10.dec 1964266T6	1222	1525
57	234137.10.dec g615414	1227	1560
57	234137.10.dec g2695401	1234	1560
57	234137.10.dec g3848367	1234	1566
57	234137.10.dec g3807796	1244	1566
57	234137.10.dec 2653885F6	511	988
57	234137.10.dec 4950523H1	511	793
57	234137.10.dec 5091884H1	519	777
57	234137.10.dec 639236H1	521	777
57	234137.10.dec 1964688H1	544	797
57	234137.10.dec 5328885H1	783	1037
57	234137.10.dec 5782346H1	783	1045
57	234137.10.dec 842587R1	807	1376
57	234137.10.dec 842587H1	807	1063
58	480630.4.dec 1696087H1	613	813
58	480630.4.dec 4922014H1	628	887
58	480630.4.dec 978059H1	639	983
58	480630.4.dec 3770059H1	646	965
58	480630.4.dec 4701108H1	655	923
58	480630.4.dec 5278092H1	610	855
58	480630.4.dec 1947038H1	663	886
58	480630.4.dec g1689331	666	733
58	480630.4.dec 1977455H1	667	915
58	480630.4.dec 4746472H1	968	1178
58	480630.4.dec 3879257H1	997	1270
58	480630.4.dec 5731570H1	1172	1418
58	480630.4.dec 4362583H1	1187	1400
58	480630.4.dec 1334076H1	1196	1425
58	480630.4.dec 2398760H1	1059	1307
58	480630.4.dec 3696394H1	1065	1334
58	480630.4.dec g1991868	1089	1473
58	480630.4.dec 201032H1	1093	1497
58	480630.4.dec g1874953	1094	1490
58	480630.4.dec 201032R1	1094	1632
58	480630.4.dec 205195H1	1094	1460
58	480630.4.dec 205569H1	1094	1329
58	480630.4.dec 1292070H1	1100	1293
58	480630.4.dec 1292070F1	1100	1664
58	480630.4.dec 2640137H1	1101	1337
58	480630.4.dec 1292276H1	1100	1333
58	480630.4.dec 5700381H1	1117	1261
58	480630.4.dec 6074887H1	1118	1418
58	480630.4.dec 5442484H1	1120	1342
58	480630.4.dec 435271H1	1130	1338
58	480630.4.dec 1400593H1	1145	1339
58	480630.4.dec 1800427H1	1160	1430
58	480630.4.dec 601700H1	1199	1448
58	480630.4.dec 2022558H1	1215	1474
58	480630.4.dec 5223360H1	1218	1485
58	480630.4.dec 5098384H1	1276	1500
58	480630.4.dec 2306363H1	1278	1541
58	480630.4.dec 6078781H1	1298	1606
58	480630.4.dec g2343652	1316	1728
58	480630.4.dec 3915833H1	1320	1615
58	480630.4.dec 5604966H1	1328	1577
58	480630.4.dec 4535083T1	1344	1904
58	480630.4.dec 2562006H1	1346	1621
58	480630.4.dec 2411212H1	1355	1559
58	480630.4.dec 1981090H1	1363	1611
58	480630.4.dec 1981090R6	1363	1858
58	480630.4.dec 1506522H1	1368	1567
58	480630.4.dec 1504651H1	1368	1614
58	480630.4.dec 1981090T6	1394	1893
58	480630.4.dec 2741376H1	1400	1655
58	480630.4.dec 1866262T6	1416	1892
58	480630.4.dec 4145756H1	1424	1748
58	480630.4.dec 3407885H1	1425	1682
58	480630.4.dec 5443335H1	1426	1673
58	480630.4.dec g2141427	1424	1788
58	480630.4.dec 5198968H1	1431	1615

Table 2 cont.

58	480630.4.dec	2793926H1	1433	1744	58	480630.4.dec	g1976684	808	1241
58	480630.4.dec	g2343629	1432	1796	58	480630.4.dec	1864125H1	831	1133
58	480630.4.dec	5490024H1	1435	1723	58	480630.4.dec	3177869H1	831	1152
58	480630.4.dec	2626277H1	1447	1673	58	480630.4.dec	925425H1	897	1202
58	480630.4.dec	3219835H1	1451	1757	58	480630.4.dec	924684R1	897	1331
58	480630.4.dec	g1390343	1450	1891	58	480630.4.dec	924684H1	898	1169
58	480630.4.dec	1803241H1	1454	1674	58	480630.4.dec	3179844H1	914	1225
58	480630.4.dec	4773772H1	1462	1725	58	480630.4.dec	5433521H1	949	1186
58	480630.4.dec	5174892H1	1468	1555	58	480630.4.dec	2553966H1	949	1223
58	480630.4.dec	4367404H1	1472	1725	58	480630.4.dec	g1445465	967	1341
58	480630.4.dec	g2837598	1475	1932	58	480630.4.dec	5044309H1	423	693
58	480630.4.dec	g4736639	1487	1938	58	480630.4.dec	2151905H1	424	676
58	480630.4.dec	g2728681	1490	1932	58	480630.4.dec	2131706H1	450	720
58	480630.4.dec	g3756314	1511	1932	58	480630.4.dec	2868958H1	458	681
58	480630.4.dec	g3330906	1508	1933	58	480630.4.dec	2106234H1	326	573
58	480630.4.dec	2758440H1	1514	1777	58	480630.4.dec	3296308H1	415	672
58	480630.4.dec	3296308T6	1517	1898	58	480630.4.dec	3296308F6	415	848
58	480630.4.dec	g2657800	1516	1932	58	480630.4.dec	g1645413	1	96
58	480630.4.dec	g4568716	1527	1932	58	480630.4.dec	1732045H1	1	284
58	480630.4.dec	g3253868	1521	1933	58	480630.4.dec	2451711H1	87	331
58	480630.4.dec	1209430T1	1534	1896	58	480630.4.dec	6603078H1	170	599
58	480630.4.dec	g4618917	1534	1932	59	480951.5.dec	2613688H1	8	249
58	480630.4.dec	g3445980	1534	1932	59	480951.5.dec	1371886H1	367	587
58	480630.4.dec	201032F1	1550	1932	59	480951.5.dec	2741956H1	367	615
58	480630.4.dec	1834212H1	1559	1834	59	480951.5.dec	3574186H1	367	637
58	480630.4.dec	1834212T6	1559	1893	59	480951.5.dec	3745122H1	378	679
58	480630.4.dec	g2219997	1572	1939	59	480951.5.dec	491592H1	380	531
58	480630.4.dec	815632H1	1579	1813	59	480951.5.dec	2441829H1	375	581
58	480630.4.dec	g2538714	1581	1944	59	480951.5.dec	6100267H1	376	663
58	480630.4.dec	g1388684	1586	1932	59	480951.5.dec	g1974420	378	725
58	480630.4.dec	g2195437	1593	1932	59	480951.5.dec	g1718741	379	663
58	480630.4.dec	2825773T6	1598	1890	59	480951.5.dec	2599377H1	366	634
58	480630.4.dec	g2161259	1611	1937	59	480951.5.dec	3331491H1	382	620
58	480630.4.dec	2460384H1	1611	1835	59	480951.5.dec	3336103H1	1167	1426
58	480630.4.dec	g4740936	1609	1940	59	480951.5.dec	3359017H1	1168	1449
58	480630.4.dec	g3213847	1615	1942	59	480951.5.dec	2508116H1	1180	1417
58	480630.4.dec	g4892585	1622	1935	59	480951.5.dec	5217308H1	1180	1420
58	480630.4.dec	g2115665	1637	1932	59	480951.5.dec	5733042H1	1217	1442
58	480630.4.dec	g315021	1659	1932	59	480951.5.dec	4115350H1	1217	1471
58	480630.4.dec	g3422567	1665	1932	59	480951.5.dec	6315280H1	1265	1435
58	480630.4.dec	g1241338	1665	1932	59	480951.5.dec	g2266304	1392	1539
58	480630.4.dec	g2779212	1668	1898	59	480951.5.dec	680479H1	1445	1607
58	480630.4.dec	g825084	1696	1942	59	480951.5.dec	3726996H1	403	691
58	480630.4.dec	g3277734	1704	1943	59	480951.5.dec	1989538H1	367	687
58	480630.4.dec	3706040H1	504	764	59	480951.5.dec	4374001H1	367	657
58	480630.4.dec	2726096H1	504	728	59	480951.5.dec	3385558H1	367	632
58	480630.4.dec	6606548H1	535	1097	59	480951.5.dec	3541978H1	18	225
58	480630.4.dec	4947185H1	569	799	59	480951.5.dec	5954134H1	806	1123
58	480630.4.dec	5202184H1	607	806	59	480951.5.dec	2780282H1	808	970
58	480630.4.dec	g3889620	1746	1939	59	480951.5.dec	5212745H1	848	1017
58	480630.4.dec	g1875009	1758	1940	59	480951.5.dec	6570768H1	868	1329
58	480630.4.dec	g2732264	1818	1942	59	480951.5.dec	2252058H1	1002	1224
58	480630.4.dec	g2007592	1851	2165	59	480951.5.dec	2020306T6	995	1498
58	480630.4.dec	g2898362	1863	1932	59	480951.5.dec	6110583H1	1002	1204
58	480630.4.dec	g3047837	1869	1932	59	480951.5.dec	2721730H1	1002	1213
58	480630.4.dec	4947804F6	773	1232	59	480951.5.dec	338780H1	1002	1193
58	480630.4.dec	1693713H1	773	1002	59	480951.5.dec	3527343H1	1008	1285
58	480630.4.dec	3576689H1	780	1074	59	480951.5.dec	6568044H1	1080	1385
58	480630.4.dec	548416H1	781	921	59	480951.5.dec	2128264H1	1098	1377
58	480630.4.dec	4992743H1	747	944	59	480951.5.dec	679425H1	1103	1361
58	480630.4.dec	4947804H1	773	874	59	480951.5.dec	630229H1	1108	1351
58	480630.4.dec	g1986962	673	940	59	480951.5.d c	2126237H1	1115	1363
58	480630.4.dec	4535083H1	670	804	59	480951.5.d c	4060761H1	1115	1380
58	480630.4.dec	g4929642	674	1944	59	480951.5.dec	546732H1	1115	1359
58	480630.4.dec	g792010	696	1021	59	480951.5.d c	378369H1	1122	1360
58	480630.4.dec	4992948H1	747	1021	59	480951.5.dec	451941H1	1124	1325
58	480630.4.dec	4992572H1	747	1009	59	480951.5.d c	4380896H1	1126	1324
58	480630.4.dec	5557064H1	747	1005	59	480951.5.dec	510978H1	1144	1360

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59	480951.5.dec	1648031H1	1149	1349
59	480951.5.dec	1648008H1	1149	1360
59	480951.5.dec	2044321H1	1150	1385
59	480951.5.dec	4216861H1	1150	1417
59	480951.5.dec	880261H1	1165	1471
59	480951.5.dec	562595H1	1166	1383
59	480951.5.dec	1579085H1	394	573
59	480951.5.dec	2742261H1	394	657
59	480951.5.dec	g1147442	397	721
59	480951.5.dec	3247844H1	409	700
59	480951.5.dec	3541674H1	408	713
59	480951.5.dec	3140608H1	409	691
59	480951.5.dec	g1972153	410	646
59	480951.5.dec	g1367340	408	805
59	480951.5.dec	5545462H1	409	605
59	480951.5.dec	g1425731	410	900
59	480951.5.dec	1988757R6	403	796
59	480951.5.dec	1988757H1	403	686
59	480951.5.dec	g1978134	403	714
59	480951.5.dec	1423332H1	403	641
59	480951.5.dec	g1068989	407	740
59	480951.5.dec	2664883H1	406	651
59	480951.5.dec	2535301H1	406	646
59	480951.5.dec	g1313751	407	720
59	480951.5.dec	1236075F1	443	1050
59	480951.5.dec	4770049H1	388	655
59	480951.5.dec	3571943H1	331	475
59	480951.5.dec	3373291H1	332	573
59	480951.5.dec	466549H1	331	531
59	480951.5.dec	5292779H2	332	582
59	480951.5.dec	3119978H1	370	639
59	480951.5.dec	2898280H1	371	577
59	480951.5.dec	g981973	372	633
59	480951.5.dec	2650347H1	362	595
59	480951.5.dec	3987391H1	362	629
59	480951.5.dec	4205158H1	362	639
59	480951.5.dec	2520140H1	369	599
59	480951.5.dec	2878674H1	370	640
59	480951.5.dec	4170133H1	370	649
59	480951.5.dec	3649034H1	370	537
59	480951.5.dec	3363180H1	370	623
59	480951.5.dec	2047646H1	370	621
59	480951.5.dec	687508H1	1445	1607
59	480951.5.dec	2235148H1	335	577
59	480951.5.dec	4891424H1	336	613
59	480951.5.dec	g2013066	334	595
59	480951.5.dec	2235148F6	335	784
59	480951.5.dec	g2035111	335	515
59	480951.5.dec	6512863H1	336	922
59	480951.5.dec	3390870H1	340	632
59	480951.5.dec	6478785H1	402	551
59	480951.5.dec	3565518H1	400	701
59	480951.5.dec	855828R1	628	1198
59	480951.5.dec	855828H1	628	853
59	480951.5.dec	5208639H1	608	874
59	480951.5.dec	g4194092	616	935
59	480951.5.dec	g892912	636	1006
59	480951.5.dec	1660116H1	635	855
59	480951.5.dec	986785H1	618	836
59	480951.5.dec	986785R1	618	1061
59	480951.5.dec	g1687504	627	1039
59	480951.5.dec	1660036H1	635	763
59	480951.5.dec	4459507H1	636	888
59	480951.5.dec	2243455H1	638	901
59	480951.5.dec	2737280H1	639	876
59	480951.5.dec	3051410H1	648	946
59	480951.5.dec	650429H1	380	614
59	480951.5.dec	5224648H1	381	481
59	480951.5.dec	6269863H1	367	896
59	480951.5.dec	1346252H1	374	593
59	480951.5.dec	3470714H1	547	806
59	480951.5.dec	3214025H1	553	801
59	480951.5.dec	037805H1	555	733
59	480951.5.dec	5401247H1	559	837
59	480951.5.dec	5410853H1	558	810
59	480951.5.dec	g4310946	601	1059
59	480951.5.dec	3111016H1	608	709
59	480951.5.dec	g3178543	603	960
59	480951.5.dec	452965H1	604	819
59	480951.5.dec	g2056998	1	223
59	480951.5.dec	6322880H1	795	970
59	480951.5.dec	999590H1	799	970
59	480951.5.dec	3758338H1	402	695
59	480951.5.dec	3326928H1	402	670
59	480951.5.dec	2729711H1	402	658
59	480951.5.dec	g1146694	403	748
59	480951.5.dec	2020306F6	403	796
59	480951.5.dec	2133705H1	401	657
59	480951.5.dec	3647806H1	402	718
59	480951.5.dec	4822653H1	401	664
59	480951.5.dec	g1625996	403	763
59	480951.5.dec	4842127H1	402	660
59	480951.5.dec	2020306H1	403	681
59	480951.5.dec	4418643H1	401	662
59	480951.5.dec	4747674H1	401	673
59	480951.5.dec	4174839H1	401	682
59	480951.5.dec	5395040H1	393	657
59	480951.5.dec	5542605H1	392	605
59	480951.5.dec	3117868H1	277	467
59	480951.5.dec	3243270H1	307	551
59	480951.5.dec	3750596H1	1	162
59	480951.5.dec	6478980H1	1	467
59	480951.5.dec	g2229512	237	648
59	480951.5.dec	5542378H1	251	437
59	480951.5.dec	3395687H1	241	487
59	480951.5.dec	3395818H1	242	533
59	480951.5.dec	6562968H1	290	812
59	480951.5.dec	4415741H1	271	525
59	480951.5.dec	6380347H1	369	685
59	480951.5.dec	3751944H1	368	569
59	480951.5.dec	4786273H2	368	548
59	480951.5.dec	3504819H1	369	671
59	480951.5.dec	g1198636	372	697
59	480951.5.dec	g2025536	372	658
59	480951.5.dec	3551711H1	372	670
59	480951.5.dec	3579019H1	701	988
59	480951.5.dec	g892899	654	929
59	480951.5.dec	2687937H1	685	926
59	480951.5.dec	376204H1	708	967
59	480951.5.dec	2271346H1	686	943
59	480951.5.dec	1672679H1	711	831
59	480951.5.dec	2839053H1	713	972
59	480951.5.dec	5283432H1	722	970
59	480951.5.dec	4575886H1	732	987
59	480951.5.dec	5661420H1	733	986
59	480951.5.dec	3291484H1	743	970
59	480951.5.dec	g1303165	752	1022
59	480951.5.dec	3984729H1	751	928
59	480951.5.dec	3678810H1	759	970
59	480951.5.dec	3441626H1	760	970
59	480951.5.dec	3674810H1	761	949
59	480951.5.dec	1909062H1	762	970
59	480951.5.dec	3322168H1	788	1064
59	480951.5.dec	754038H1	793	970
59	480951.5.dec	1727177H1	793	970
59	480951.5.dec	5516018H1	793	970

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59	480951.5.dec	5589241H1	390	611	60	350399.5.dec	5119208H1	31	322
59	480951.5.dec	g2166364	390	767	60	350399.5.dec	4968666H1	38	167
59	480951.5.d c	1236401F6	443	871	60	350399.5.dec	4956016H1	18	120
59	480951.5.dec	5577131H1	448	701	60	350399.5.dec	4515864H1	21	216
59	480951.5.dec	g1163670	449	608	60	350399.5.dec	3215683H1	25	294
59	480951.5.dec	2779615H1	475	732	60	350399.5.dec	4511482H1	1566	1822
59	480951.5.dec	3211910H1	477	597	60	350399.5.dec	2909383H1	1567	1828
59	480951.5.dec	5615524H1	501	808	60	350399.5.dec	g4392449	1572	1941
59	480951.5.dec	2705619H1	492	753	60	350399.5.dec	6023589H1	1586	1855
59	480951.5.dec	2544567H2	526	783	60	350399.5.dec	2137195H1	1627	1852
59	480951.5.dec	1592175H1	534	730	60	350399.5.dec	4824771H1	1318	1566
59	480951.5.dec	4176769H1	535	710	60	350399.5.dec	g3678597	1337	1727
59	480951.5.dec	1591703H1	534	728	60	350399.5.dec	2486926H2	1386	1624
59	480951.5.dec	g1278591	492	637	60	350399.5.dec	1289520T6	3923	4170
59	480951.5.dec	g1156402	537	763	60	350399.5.dec	1289520F6	3923	4219
59	480951.5.dec	g1670312	491	742	60	350399.5.dec	g4109131	3931	4211
59	480951.5.dec	g1494000	492	657	60	350399.5.dec	4351280H1	3943	4211
59	480951.5.dec	g1721860	492	889	60	350399.5.dec	4432226H1	4	262
59	480951.5.dec	g989068	501	757	60	350399.5.dec	6380386H1	8	319
59	480951.5.dec	3800372H1	367	651	60	350399.5.dec	5498050H1	15	259
59	480951.5.dec	2448255H1	367	598	60	350399.5.dec	1860316H1	1270	1490
59	480951.5.dec	3765155H1	367	676	60	350399.5.dec	g1062524	3959	4199
59	480951.5.dec	6374408H1	367	606	60	350399.5.dec	g3151950	3971	4216
59	480951.5.dec	5538463H2	366	555	60	350399.5.dec	g4292288	3972	4213
59	480951.5.dec	2921720H1	380	641	60	350399.5.dec	g4888572	3975	4211
59	480951.5.dec	g2057109	160	442	60	350399.5.dec	g3155094	3986	4213
59	480951.5.dec	6481690H1	361	892	60	350399.5.dec	g1062503	3996	4186
59	480951.5.dec	595420H1	362	604	60	350399.5.dec	1602855H1	184	379
59	480951.5.dec	3591022H1	361	660	60	350399.5.dec	2716719H1	184	433
59	480951.5.dec	1320037H1	362	625	60	350399.5.dec	1300839T6	1821	2141
59	480951.5.dec	3593512H1	362	680	60	350399.5.dec	g5366860	1838	2179
59	480951.5.dec	5391147H1	362	657	60	350399.5.dec	g5630541	1865	2172
59	480951.5.dec	2719839H1	362	612	60	350399.5.dec	3523889H1	1537	1846
59	480951.5.dec	g1277584	354	847	60	350399.5.dec	355153H1	1553	1718
59	480951.5.dec	2457980H1	359	591	60	350399.5.dec	g4833913	3956	4213
59	480951.5.dec	g1799076	359	819	60	350399.5.dec	4750324H1	972	1083
59	480951.5.dec	5538138H1	361	516	60	350399.5.dec	g872980	998	1323
59	480951.5.dec	4023870H1	342	601	60	350399.5.dec	1300839H1	897	1172
59	480951.5.dec	1360005H1	342	581	60	350399.5.dec	5515034H1	915	1111
59	480951.5.dec	g1998895	343	503	60	350399.5.dec	097987H1	926	975
59	480951.5.dec	4161775H1	343	585	60	350399.5.dec	g839057	935	1323
59	480951.5.dec	3778265H1	342	647	60	350399.5.dec	2553277H1	796	1058
59	480951.5.dec	4843784H1	345	615	60	350399.5.dec	g2838628	810	1289
59	480951.5.dec	3533957H1	347	657	60	350399.5.dec	3489831H1	859	1131
59	480951.5.dec	4520442H1	349	604	60	350399.5.dec	g3148335	879	1034
59	480951.5.dec	g2669182	350	780	60	350399.5.dec	1300839F6	897	1342
59	480951.5.dec	4618672H1	349	592	60	350399.5.dec	g4486333	899	1289
59	480951.5.dec	4031302H1	342	592	60	350399.5.dec	3420362H1	4053	4211
59	480951.5.dec	3321371H1	354	632	60	350399.5.dec	3560750H1	4026	4206
59	480951.5.dec	4729423H1	355	513	60	350399.5.dec	g1551605	4054	4212
59	480951.5.dec	2581094H1	355	588	60	350399.5.dec	535434H1	4079	4211
59	480951.5.dec	3250802H1	341	642	60	350399.5.dec	g1812272	4113	4376
59	480951.5.dec	2913426H1	342	600	60	350399.5.dec	3899577H1	1	168
59	480951.5.dec	1360005F1	342	828	60	350399.5.dec	2546733H1	1	228
59	480951.5.dec	4770833H1	341	602	60	350399.5.dec	3205796H1	1	128
59	480951.5.dec	5395039H1	366	630	60	350399.5.dec	5280436H1	1	222
59	480951.5.dec	4067217H1	365	632	60	350399.5.dec	2960636H1	333	619
59	480951.5.dec	4160969H1	364	644	60	350399.5.dec	1391509H1	338	623
59	480951.5.dec	3538760H1	363	573	60	350399.5.dec	1400280H1	1126	1356
59	480951.5.dec	5064082H1	364	575	60	350399.5.dec	4387268H1	1135	1392
59	480951.5.dec	407591H1	363	520	60	350399.5.dec	g670409	1140	1306
59	480951.5.dec	5542680H1	363	579	60	350399.5.dec	g692250	1149	1297
59	480951.5.dec	3394195H1	364	627	60	350399.5.dec	1579183H1	1248	1423
59	480951.5.dec	2885143H1	364	622	60	350399.5.dec	1274218H1	1425	1658
60	350399.5.dec	3889877H1	117	388	60	350399.5.dec	g1062502	1438	1700
60	350399.5.dec	6219217H1	155	255	60	350399.5.dec	g1062523	1439	1733
60	350399.5.dec	g1784403	102	397	60	350399.5.dec	5510701H1	1451	1542
60	350399.5.dec	g1665816	26	4211	60	350399.5.dec	5407906H1	1875	2083

Table 2 cont.

60	350399.5.dec	2793202H1	1889	2180
60	350399.5.dec	5006864H1	1917	2040
60	350399.5.dec	g3190700	1968	2190
60	350399.5.dec	1865380H1	1988	2224
60	350399.5.dec	g2833914	2007	2179
60	350399.5.dec	4068580T6	2044	2135
60	350399.5.dec	6452027H1	2057	2183
60	350399.5.dec	3800286H1	2077	2183
60	350399.5.dec	3718618H1	2123	2421
60	350399.5.dec	2151703H1	2128	2403
60	350399.5.dec	3461351H1	2956	3201
60	350399.5.dec	g1551504	2219	2436
60	350399.5.dec	2223501H1	2219	2446
60	350399.5.dec	g827589	2276	2455
60	350399.5.dec	g2064407	2312	2724
60	350399.5.dec	g1812596	2325	2438
60	350399.5.dec	2883116H1	2324	2616
60	350399.5.dec	g1812756	2326	2565
60	350399.5.dec	5698841H1	2326	2573
60	350399.5.dec	2292715H1	2333	2624
60	350399.5.dec	1719208F6	2402	2715
60	350399.5.dec	2821690H1	2412	2708
60	350399.5.dec	2824732H1	2412	2712
60	350399.5.dec	2289458H1	2496	2627
60	350399.5.dec	2877589H1	2508	2788
60	350399.5.dec	1719208H1	2519	2712
60	350399.5.dec	4537301H1	2540	2793
60	350399.5.dec	3290129H1	2542	2783
60	350399.5.dec	695895H1	2558	2782
60	350399.5.dec	g5363819	2561	2712
60	350399.5.dec	6314465H1	2598	3152
60	350399.5.dec	4920360H1	2650	2930
60	350399.5.dec	3504502H1	2702	2902
60	350399.5.dec	4630083H1	2759	2824
60	350399.5.dec	2814355F6	2765	3328
60	350399.5.dec	2814355H1	2765	3073
60	350399.5.dec	3452209H1	2979	3238
60	350399.5.dec	2843473H1	2795	3063
60	350399.5.dec	6411224H1	3034	3307
60	350399.5.dec	4994153H1	2798	2950
60	350399.5.dec	3685334H1	2803	3106
60	350399.5.dec	1431740R6	2862	3337
60	350399.5.dec	1431740H1	2862	3070
60	350399.5.dec	1431740R1	2862	3144
60	350399.5.dec	2447927H1	2942	3178
60	350399.5.dec	2447927F6	2942	3428
60	350399.5.dec	3446015H1	2954	3073
60	350399.5.dec	5372158H1	2955	3180
60	350399.5.dec	1619598H1	2956	3154
60	350399.5.dec	664175H1	3037	3282
60	350399.5.dec	6408282H1	3043	3567
60	350399.5.dec	g1271956	3060	3410
60	350399.5.dec	3134408H1	3061	3335
60	350399.5.dec	3255616H1	3104	3360
60	350399.5.dec	4089831H1	3182	3458
60	350399.5.dec	g3255048	3211	3596
60	350399.5.dec	5352165H1	3213	3315
60	350399.5.dec	1995825H1	3217	3484
60	350399.5.dec	4934215H1	3219	3460
60	350399.5.dec	2459559H1	3247	3476
60	350399.5.dec	1620983F6	3265	3745
60	350399.5.dec	1620983H1	3265	3485
60	350399.5.dec	5103592H1	3281	3492
60	350399.5.dec	1859304F6	3291	3815
60	350399.5.dec	1859303H1	3291	3562
60	350399.5.dec	6614830H1	3339	3879
60	350399.5.dec	1894769H1	3381	3630
60	350399.5.d c	4630494H1	3395	3655
60	350399.5.dec	4630611H1	3395	3650
60	350399.5.dec	2896677H1	3418	3605
60	350399.5.dec	g1812383	3468	3754
60	350399.5.dec	1740387H1	3473	3694
60	350399.5.dec	1740387R6	3473	3862
60	350399.5.dec	4061120H1	3473	3747
60	350399.5.dec	2695862H1	3475	3781
60	350399.5.dec	g4394313	3483	3930
60	350399.5.dec	g1549572	3505	3789
60	350399.5.dec	5865858H1	3516	3787
60	350399.5.dec	2588568H1	3520	3757
60	350399.5.dec	g2732861	3524	3748
60	350399.5.dec	2549865H1	3541	3787
60	350399.5.dec	1266266H1	3541	3774
60	350399.5.dec	g2555617	3575	3919
60	350399.5.dec	g1300483	3577	4025
60	350399.5.dec	2955496H1	3580	3848
60	350399.5.dec	2447927T6	3593	4173
60	350399.5.dec	2292715T6	3592	4172
60	350399.5.dec	5059812H1	3597	3907
60	350399.5.dec	6394265H1	3604	3820
60	350399.5.dec	2814355T6	3639	4168
60	350399.5.dec	5877319H1	3644	3917
60	350399.5.dec	4087702H1	3647	3928
60	350399.5.dec	1005310H1	3665	3934
60	350399.5.dec	5861292H1	3741	4031
60	350399.5.dec	1859304T6	3749	4174
60	350399.5.dec	g4650781	3779	4209
60	350399.5.dec	g3742022	3779	4220
60	350399.5.dec	g4264942	3790	4211
60	350399.5.dec	5206350H1	3798	4021
60	350399.5.dec	g4738038	3799	4209
60	350399.5.dec	g3649493	3803	4220
60	350399.5.dec	1431740T6	3808	4168
60	350399.5.dec	g3539316	3812	4215
60	350399.5.dec	g3539304	3812	4213
60	350399.5.dec	1637463T6	3822	4170
60	350399.5.dec	5949046H1	3823	4074
60	350399.5.dec	1620983T6	3830	4190
60	350399.5.dec	1637463F6	3829	4183
60	350399.5.dec	1637463H1	3829	4043
60	350399.5.dec	g1549797	3830	4211
60	350399.5.dec	g2069536	3829	4209
60	350399.5.dec	g2942270	3829	4216
60	350399.5.dec	g4186986	3830	4211
60	350399.5.dec	g2942265	3830	4211
60	350399.5.dec	g3250503	3832	4209
60	350399.5.dec	g4114971	3832	4211
60	350399.5.dec	g3092120	3832	4215
60	350399.5.dec	g4089641	3833	4211
60	350399.5.dec	g4175757	3836	4211
60	350399.5.dec	940848T1	3843	4168
60	350399.5.dec	940848R1	3855	4208
60	350399.5.dec	940848H1	3855	4149
60	350399.5.dec	g907438	3860	4212
60	350399.5.dec	1740387T6	3858	4167
60	350399.5.dec	g2841410	3873	4216
60	350399.5.dec	g3658706	3876	4210
60	350399.5.dec	959456R1	3882	4211
60	350399.5.dec	959456H1	3882	4196
60	350399.5.dec	g5662181	3882	4218
60	350399.5.d c	g4296167	3905	4209
60	350399.5.dec	g3675020	3921	4211
60	350399.5.d c	1289520H1	3923	4173
60	350399.5.dec	3040875H1	3923	4204
60	350399.5.dec	1474180T1	1481	1688
60	350399.5.dec	1474180H1	1481	1721
60	350399.5.dec	112663T6	1496	1669

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60	350399.5.dec	3941003H1	1528	1695	61	085713.2.dec	3927329H1	1611	1877
60	350399.5.dec	4672530H1	291	563	61	085713.2.dec	2593752H1	1634	1824
60	350399.5.dec	g1471517	532	1001	61	085713.2.dec	g1981200	1636	1923
60	350399.5.dec	g751699	533	745	61	085713.2.dec	2097957H1	1581	1857
60	350399.5.dec	g692289	534	754	61	085713.2.dec	3769037H1	1589	1843
60	350399.5.dec	g714847	610	823	61	085713.2.dec	1683135H1	1712	1852
60	350399.5.dec	112663R6	619	1121	61	085713.2.dec	3509114H1	1593	1863
60	350399.5.dec	112663H1	619	776	61	085713.2.dec	5832853H1	1747	2024
60	350399.5.dec	3719539H1	694	972	61	085713.2.dec	806178H1	1751	1977
60	350399.5.dec	2844152H1	1388	1660	61	085713.2.dec	3558496H1	1759	2028
60	350399.5.dec	5347842H1	1399	1589	61	085713.2.dec	2795155H1	1798	2044
60	350399.5.dec	6494421H1	1418	1873	61	085713.2.dec	1982603R6	1822	2270
60	350399.5.dec	g3003587	1418	1676	61	085713.2.dec	2902677H1	1159	1455
60	350399.5.dec	1274218F1	1425	1850	61	085713.2.dec	g4451382	1071	1388
60	350399.5.dec	3409696H1	1742	1964	61	085713.2.dec	g316154	1145	1429
60	350399.5.dec	g3645371	1742	2179	61	085713.2.dec	5819630H1	1190	1501
60	350399.5.dec	4532952H1	1745	1936	61	085713.2.dec	2869957H1	622	901
60	350399.5.dec	1879147H1	1745	1905	61	085713.2.dec	2869957F6	622	1183
60	350399.5.dec	3719622H1	1777	2067	61	085713.2.dec	g942739	631	910
60	350399.5.dec	g3425750	1776	2187	61	085713.2.dec	g1477126	642	1075
60	350399.5.dec	g3213638	1784	2182	61	085713.2.dec	g1527541	642	1024
60	350399.5.dec	g1784345	1802	2179	61	085713.2.dec	g969342	642	761
60	350399.5.dec	4376792H1	1726	1968	61	085713.2.dec	g2184408	680	1130
60	350399.5.dec	4376541H1	1725	1964	61	085713.2.dec	5307452H1	722	974
60	350399.5.dec	4128636H1	1736	1865	61	085713.2.dec	6321277H1	924	1168
60	350399.5.dec	g566326	1054	1306	61	085713.2.dec	2869957T6	805	1349
60	350399.5.dec	g751651	1061	1296	61	085713.2.dec	g2037747	845	1154
60	350399.5.dec	g814715	1075	1310	61	085713.2.dec	2463542H1	924	1143
60	350399.5.dec	5095975H2	1108	1307	61	085713.2.dec	2463542F6	924	1471
60	350399.5.dec	g1471430	1106	1289	61	085713.2.dec	2044369H1	2147	2382
60	350399.5.dec	1382644H1	1126	1374	61	085713.2.dec	1772731H1	2199	2416
60	350399.5.dec	6387138H1	346	636	61	085713.2.dec	4266001H1	2234	2423
60	350399.5.dec	5833550H1	430	629	61	085713.2.dec	4730142H1	2259	2513
60	350399.5.dec	2723562H1	443	688	61	085713.2.dec	g2555947	2264	2571
60	350399.5.dec	5413045H1	496	637	61	085713.2.dec	840781H1	2265	2537
60	350399.5.dec	3451343H1	501	741	61	085713.2.dec	4593969H1	2265	2534
61	085713.2.dec	2876519H1	1838	2093	61	085713.2.dec	g5109339	2281	2739
61	085713.2.dec	g3804453	1850	2282	61	085713.2.dec	5821366H1	1190	1509
61	085713.2.dec	4714518H1	1862	1946	61	085713.2.dec	5818829H1	1190	1413
61	085713.2.dec	g4522739	1882	2281	61	085713.2.dec	5813545H1	1190	1448
61	085713.2.dec	g5369593	1907	2378	61	085713.2.dec	5817650H1	1190	1357
61	085713.2.dec	5563230H1	1914	2142	61	085713.2.dec	5812917H1	1190	1464
61	085713.2.dec	5327933H1	1919	2180	61	085713.2.dec	6518401H1	761	1303
61	085713.2.dec	g3658839	1938	2349	61	085713.2.dec	2655535T6	723	1339
61	085713.2.dec	g3927414	1943	2378	61	085713.2.dec	5910362H1	601	903
61	085713.2.dec	5275308H1	1960	2193	61	085713.2.dec	2878073H1	2532	2739
61	085713.2.dec	2673389H1	2002	2250	61	085713.2.dec	g944173	2537	2634
61	085713.2.dec	5333974H1	2009	2257	61	085713.2.dec	3702759H1	2549	2737
61	085713.2.dec	1982603H1	2046	2270	61	085713.2.dec	g5325988	2549	2737
61	085713.2.dec	4726834H1	2147	2424	61	085713.2.dec	g969343	2585	2737
61	085713.2.dec	g4196655	2147	2282	61	085713.2.dec	2043940H1	2606	2737
61	085713.2.dec	3484912H1	962	1297	61	085713.2.dec	661586H1	2613	2768
61	085713.2.dec	2552885T6	980	1345	61	085713.2.dec	5056769H1	2657	2744
61	085713.2.dec	552697H1	934	1162	61	085713.2.dec	6306802H1	1347	1705
61	085713.2.dec	g2594419	997	1387	61	085713.2.dec	3042074H1	1426	1741
61	085713.2.dec	g1647965	1041	1363	61	085713.2.dec	4261452H1	1429	1688
61	085713.2.dec	613645H1	2292	2526	61	085713.2.dec	2773951H1	1443	1697
61	085713.2.dec	2132842H1	2331	2572	61	085713.2.dec	g3050704	1463	1658
61	085713.2.dec	g4073710	2339	2740	61	085713.2.dec	6023537H1	1482	1718
61	085713.2.dec	g1527498	2368	2738	61	085713.2.dec	2653867H1	1489	1775
61	085713.2.dec	g2184179	2408	2740	61	085713.2.dec	5412976H1	1525	1780
61	085713.2.dec	2721848H1	2411	2662	61	085713.2.dec	g3960542	1535	1796
61	085713.2.dec	2637714H1	2411	2664	61	085713.2.d c	g1119058	1546	1671
61	085713.2.dec	g274328	2412	2737	61	085713.2.dec	6411539H1	1571	2071
61	085713.2.dec	3801333H1	1	282	61	085713.2.dec	g3077101	1298	1676
61	085713.2.dec	2857263F6	608	1073	61	085713.2.dec	g2958693	1313	1675
61	085713.2.dec	2857263H1	608	721	61	085713.2.dec	3640567H1	1329	1534
61	085713.2.dec	6212439H1	610	893	61	085713.2.dec	g2569732	1337	1749

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61	085713.2.dec	2267280H1	1338	1550
61	085713.2.dec	5814634H1	1190	1515
61	085713.2.d c	5817645H1	1190	1517
61	085713.2.dec	5822469H1	1189	1441
61	085713.2.dec	5816778H1	1190	1504
61	085713.2.dec	g4295078	1197	1388
61	085713.2.dec	2463542T6	1243	1724
61	085713.2.dec	g1982163	1296	1526
61	085713.2.dec	g867230	2438	2737
61	085713.2.dec	g1477035	2474	2738
61	085713.2.dec	646057H1	2485	2739
61	085713.2.dec	6158466H1	2485	2647
61	085713.2.dec	3535428H1	2505	2737
61	085713.2.dec	g1479354	2517	2736
61	085713.2.dec	g3095823	2528	2661
61	085713.2.dec	4096762H1	371	676
61	085713.2.dec	4510286H1	410	660
61	085713.2.dec	007733H1	485	754
61	085713.2.dec	3021452H1	158	454
61	085713.2.dec	2655535H1	181	475
61	085713.2.dec	2655535F6	181	610
61	085713.2.dec	2655535F7	181	604
61	085713.2.dec	1902994H1	336	585
62	245014.1.dec	6345408H1	611	884
62	245014.1.dec	4435621H1	722	996
62	245014.1.dec	4439530H1	634	878
62	245014.1.dec	4972429H1	680	969
62	245014.1.dec	3275925H1	732	970
62	245014.1.dec	g3446618	733	1187
62	245014.1.dec	5299476H1	733	883
62	245014.1.dec	g2541414	741	1184
62	245014.1.dec	4602871H1	755	1002
62	245014.1.dec	2884645H1	762	1025
62	245014.1.dec	4196193H1	857	991
62	245014.1.dec	g2139409	871	1261
62	245014.1.dec	2872604H1	874	1135
62	245014.1.dec	4212104H1	921	1189
62	245014.1.dec	g4901006	896	956
62	245014.1.dec	960167H1	1044	1167
62	245014.1.dec	3450361R6	68	532
62	245014.1.dec	5399133H1	1	210
62	245014.1.dec	3450361H1	68	323
62	245014.1.dec	2731452F6	81	415
62	245014.1.dec	2731452H1	81	316
62	245014.1.dec	263691H1	94	421
62	245014.1.dec	5674201H1	106	342
62	245014.1.dec	2645021H1	204	452
62	245014.1.dec	6452902H1	207	656
62	245014.1.dec	g895569	341	502
62	245014.1.dec	4797535H1	355	637
62	245014.1.dec	4164512H1	362	662
62	245014.1.dec	g1128352	368	601
62	245014.1.dec	g2003284	449	699
62	245014.1.dec	6513260H1	519	1008
62	245014.1.dec	g878573	536	855
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Table 3

SEQ ID NO	Template ID	Tissue Distribution
1	198450.6.oct	Embryonic Structures - 17%, Germ Cells - 16%, Cardiovascular System - 13%
2	475178.1.oct	Sense Organs - 44%, Unclassified/Mixed - 20%, Connective Tissue - 11%
3	231793.2.oct	Germ Cells - 29%, Digestive System - 12%, Embryonic Structures - 11%
4	000010.4.oct	Stomatognathic System - 21%, Germ Cells - 15%
5	412959.6.oct	Unclassified/Mixed - 24%, Stomatognathic System - 20%
6	331521.5.oct	Embryonic Structures - 21%
7	902114.1.oct	Skin - 41%, Musculoskeletal System - 20%, Female Genitalia - 17%, Hemic and Immune System - 17%
8	481382.1.oct	Exocrine Glands - 22%, Connective Tissue - 15%, Musculoskeletal System - 14%, Hemic and Immune System - 14%
9	903849.1.oct	Skin - 14%, Cardiovascular System - 11%
10	433776.4.oct	Male Genitalia - 15%, Endocrine System - 10%
11	407607.4.oct	Unclassified/Mixed - 19%, Pancreas - 14%, Female Genitalia - 10%
12	234828.6.oct	Liver - 16%, Endocrine System - 12%
14	242269.2.dec	Stomatognathic System - 54%, Musculoskeletal System - 18%
16	198060.6.dec	Hemic and Immune System - 100%
18	235983.6.dec	Nervous System - 100%
20	038751.5.dec	Pancreas - 100%
21	236099.4.dec	Unclassified/Mixed - 10%
23	466521.5.dec	Female Genitalia - 50%, Hemic and Immune System - 50%
24	466521.6.dec	Urinary Tract - 32%, Exocrine Glands - 14%, Cardiovascular System - 14%
25	474522.8.dec	Exocrine Glands - 31%, Urinary Tract - 31%, Digestive System - 23%
26	231583.3.dec	Sense Organs - 19%
28	277726.5.dec	Nervous System - 50%, Digestive System - 50%
29	978637.1.dec	Embryonic Structures - 29%, Nervous System - 24%, Connective Tissue - 19%
31	413231.8.dec	Female Genitalia - 16%, Respiratory System - 15%, Connective Tissue - 14%
32	334406.5.dec	Urinary Tract - 100%
33	411429.8.dec	Urinary Tract - 100%
34	320674.7.dec	Endocrine System - 32%, Skin - 25%, Connective Tissue - 12%, Cardiovascular System - 12%, Exocrine Glands - 12%
36	332335.1.dec	Digestive System - 24%, Skin - 21%, Liver - 17%
37	238992.13.dec	Digestive System - 100%
38	199736.1.dec	Urinary Tract - 25%, Pancreas - 22%, Male Genitalia - 14%
39	228864.5.dec	Nervous System - 100%
40	986539.1.dec	Skin - 24%, Embryonic Structures - 17%, Hemic and Immune System - 16%, Unclassified/Mixed - 16%
41	481454.4.dec	Musculoskeletal System - 53%, Sense Organs - 42%
42	474800.7.dec	Male Genitalia - 100%
45	353271.2.dec	Female Genitalia - 25%, Digestive System - 25%, Hemic and Immune System - 25%
46	221686.2.dec	Embryonic Structures - 12%, Endocrine System - 11%, Unclassified/Mixed - 10%
47	233347.7.dec	Stomatognathic System - 73%
48	230631.3.dec	Embryonic Structures - 100%
50	337160.1.dec	Embryonic Structures - 22%, Unclassified/Mixed - 20%, Urinary Tract - 19%
51	346341.12.dec	Embryonic Structures - 11%, Germ Cells - 11%

Table 3 cont.

SEQ ID NO	Template ID	Tissue Distribution
52	428745.2.dec	Hemic and Immune System - 100%
53	444839.17.dec	Musculoskeletal System - 70%, Female Genitalia - 30%
55	428362.36.dec	Embryonic Structures - 34%, Connective Tissue - 24%, Liver - 18%
56	480710.12.dec	Urinary Tract - 33%, Nervous System - 25%, Digestive System - 25%
57	234137.10.dec	Skin - 59%, Endocrine System - 21%, Digestive System - 10%, Hemic and Immune System - 10%
58	480630.4.dec	Hemic and Immune System - 67%, Nervous System - 33%
60	350399.5.dec	Unclassified/Mixed - 100%
61	085713.2.dec	Cardiovascular System - 29%, Urinary Tract - 29%, Female Genitalia - 21%
63	117464.7.dec	Skin - 25%, Endocrine System - 13%

Table 4

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	PE Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	PE Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	PE Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25:3389-3402.	*ESTs:* Probability value= 1.0E-8 or less *Full Length sequences*: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises as least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad Sci. USA 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183:63-98; and Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489.	*ESTs:* fasta E value=1.06E-6 *Assembled ESTs*: fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less *Full Length sequences:* fastx score=100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff (1991) Nucleic Acids Res. 19:6565-6572; Henikoff, J.G. and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37:417-424.	Score=1000 or greater; Ratio of Score/Strength = 0.75 or larger; and, if applicable, Probability value= 1.0E-3 or less
HMMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM.	Krogh, A. et al. (1994) J. Mol. Biol. 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322.	Score=10-50 bits for PFAM hits, depending on individual protein families

Table 4 (cont.)

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, M. et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221.	Normalized quality score≥GCG-specified "HIGH" value for that particular Prosite motif. Generally, score=1.4-2.1.
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M.S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies.	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12:431-439.	Score=3.5 or greater
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

CLAIMS

What is claimed is:

1. An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:

a) a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63,

b) a naturally occurring polynucleotide sequence having at least 90% sequence identity to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63,

c) a polynucleotide sequence complementary to a),

d) a polynucleotide sequence complementary to b), and

e) an RNA equivalent of a) through d).

2. An isolated polynucleotide of claim 1, comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-63.

3. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide of claim 1.

4. A composition for the detection of expression of secretory polynucleotides comprising at least one of the polynucleotides of claim 1 and a detectable label.

5. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 1, the method comprising:

a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and

b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

6. A method for detecting a target polynucleotide in a sample, said target polynucleotide comprising a sequence of a polynucleotide of claim 1, the method comprising:

a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and

b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

7. A method of claim 5, wherein the probe comprises at least 30 contiguous nucleotides.

8. A method of claim 5, wherein the probe comprises at least 60 contiguous nucleotides.

9. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 1.

10. A cell transformed with a recombinant polynucleotide of claim 9.

11. A transgenic organism comprising a recombinant polynucleotide of claim 9.

12. A method for producing a secretory polypeptide, the method comprising:

a) culturing a cell under conditions suitable for expression of the secretory polypeptide, wherein said cell is transformed with a recombinant polynucleotide of claim 9, and

b) recovering the secretory polypeptide so expressed.

13. A purified secretory polypeptide encoded by at least one of the polynucleotides of claim 2.

14. An isolated antibody which specifically binds to a secretory polypeptide of claim 13.

15. A method of identifying a test compound which specifically binds to the secretory polypeptide of claim 13, the method comprising the steps of:

a) providing a test compound;

b) combining the secretory polypeptide with the test compound for a sufficient time and under suitable conditions for binding; and

c) detecting binding of the secretory polypeptide to the test compound, thereby identifying the test compound which specifically binds the secretory polypeptide.

16. A microarray wherein at least one element of the microarray is a polynucleotide of claim 3.

17. A method for generating a transcript image of a sample which contains polynucleotides, the method comprising the steps of:

a) labeling the polynucleotides of the sample,

b) contacting the elements of the microarray of claim 16 with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and

c) quantifying the expression of the polynucleotides in the sample.

18. A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a polynucleotide sequence of claim 1, the method comprising:

a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,

b) detecting altered expression of the target polynucleotide, and

c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

19. A method for assessing toxicity of a test compound, said method comprising:

a) treating a biological sample containing nucleic acids with the test compound;

b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 1 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 1 or fragment thereof;

c) quantifying the amount of hybridization complex; and

d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

SEQUENCE LISTING

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LINCOLN, Stephen E.
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SPIRO, Peter A.
BANVILLE, Steve C.
BRATCHER, Shawn R.
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SHAH, Purvi
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HILLMAN, Jennifer L.
JONES, Anissa L.
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ROSEBERRY, Ann M.
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<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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<223> Incyte ID No: 412959.6.oct

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<220>
<221> unsure

<222> 276
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<211> 985
<212> DNA
<213> Homo sapiens

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<220>
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<222> 456, 460-461, 470, 772, 805, 913, 945, 958, 982
<223> a, t, c, g, or other

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<210> 8
<211> 848
<212> DNA
<213> Homo sapiens

<220>
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<223> Incyte ID No: 481382.1.oct

<220>
<221> unsure
<222> 787, 837
<223> a, t, c, g, or other

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<211> 1615
<212> DNA
<213> Homo sapiens

<220>
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<223> Incyte ID No: 903849.1.oct

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<210> 10
<211> 942
<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 433776.4.oct

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<210> 11
<211> 1728
<212> DNA
<213> Homo sapiens

<220>
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<223> Incyte ID No: 407607.4.oct

<220>
<221> unsure
<222> 26, 79
<223> a, t, c, g, or other

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<213> Homo sapiens

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<213> Homo sapiens

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<222> 74
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<213> Homo sapiens

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<213> Homo sapiens

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<222> 611, 621
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<211> 4541
<212> DNA
<213> Homo sapiens

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<223> Incyte ID No: 235983.6.dec

<220>
<221> unsure
<222> 933
<223> a, t, c, g, or other

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<211> 1975
<212> DNA
<213> Homo sapiens

<220>
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<223> Incyte ID No: 236099.4.dec

<220>
<221> unsure
<222> 1856, 1891, 1901, 1951, 1953, 1968
<223> a, t, c, g, or other

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gcaccgtggt ccagcagagg cgctgggtgg nagggcacgc nggcaagcct aggagagtag 1920
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<210> 22
<211> 1028
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 350875.2.dec

<220>
<221> unsure
<222> 237, 242, 251, 255
<223> a, t, c, g, or other

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gntgacgatg ntgangagcc aatctttgtt ggcgagatat caagttcaaa accagcaatt 300
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tgtataag 1028

<210> 23
<211> 673
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 466521.5.dec

<400> 23
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ggtaaccaga acagagagct gtaaactccg tgaatgcaag aggctgcttc tgttacctga 360
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tcttatactc tcacaggtag aatgaactgt gtactggcca catatggaag cattgcattg 540
attgtcttat atttcaagtt aaggtccaaa aaaactccag ctgtgaaagc aacataaatg 600
gattttaaac tgtctacggt tcttaacctc atctgttaag ttcccatgcc tggagaagct 660
aatgccaact cat 673

<210> 24
<211> 834
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 466521.6.dec

<220>
<221> unsure
<222> 440
<223> a, t, c, g, or other

<400> 24

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<210> 25
<211> 1471
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 474522.8.dec

<400> 25
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<210> 26
<211> 1358
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 231583.3.dec

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<210> 27
<211> 1977
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 215051.5.dec

<220>
<221> unsure
<222> 151
<223> a, t, c, g, or other

<400> 27
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<210> 28
<211> 1447
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 277726.5.dec

<220>
<221> unsure
<222> 1428
<223> a, t, c, g, or other

<400> 28
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<210> 29
<211> 650
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 978637.1.dec

<220>
<221> unsure
<222> 400
<223> a, t, c, g, or other

<400> 29
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<212> DNA
<213> Homo sapiens

<220>
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<213> Homo sapiens

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<220>
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<222> 1103, 1115
<223> a, t, c, g, or other

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<213> Homo sapiens

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<211> 1231
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<213> Homo sapiens

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<210> 38
<211> 940
<212> DNA
<213> Homo sapiens

<220>
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<223> Incyte ID No: 199736.1.dec

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<211> 757
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 228864.5.dec

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<211> 1240
<212> DNA
<213> Homo sapiens

<220>
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<223> Incyte ID No: 986539.1.dec

<220>
<221> unsure
<222> 223
<223> a, t, c, g, or other

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<210> 41
<211> 2413
<212> DNA
<213> Homo sapiens

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<223> Incyte ID No: 481454.4.dec

<220>
<221> unsure
<222> 309-314, 317
<223> a, t, c, g, or other

<400> 41

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<212> DNA
<213> Homo sapiens

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<211> 680
<212> DNA
<213> Homo sapiens

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<210> 44
<211> 578
<212> DNA
<213> Homo sapiens

<220>
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<223> Incyte ID No: 018945.1.dec

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<210> 45
<211> 1075
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 353271.2.dec

<220>
<221> unsure
<222> 156, 162, 164
<223> a, t, c, g, or other

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<210> 46
<211> 1654
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 221686.2.dec

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<212> DNA
<213> Homo sapiens

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<213> Homo sapiens

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<223> a, t, c, g, or other

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<212> DNA
<213> Homo sapiens

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<220>
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<222> 991
<223> a, t, c, g, or other

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<211> 4219
<212> DNA
<213> Homo sapiens

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